

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Cys Gly Asn Leu Thr Gly Asn Ser Lys Lys Ala Ala Asp Ser Gly Asp
 1 5 10 15
 Lys Pro Val Ile Lys Met Tyr Gln Ile Gly Asp Lys Pro Asp Asn Leu
 20 25 30
 Asp Glu Leu Leu Ala Asn Ala Asn Lys Ile Ile Glu Glu Lys Val Gly
 35 40 45
 Ala Lys Leu Asp Ile Gln Tyr Leu Gly Trp Gly Asp Tyr Gly Lys Lys
 50 55 60
 Met Ser Val Ile Thr Ser Ser Gly Glu Asn Tyr Asp Ile Ala Phe Ala
 65 70 75 80
 Asp Asn Tyr Ile Val Asn Ala Gln Lys Gly Ala Tyr Ala Asp Leu Thr
 85 90 95
 Glu Leu Tyr Lys Lys Glu Gly Lys Asp Leu Tyr Lys Ala Leu Asp Pro
 100 105 110
 Ala Tyr Ile Lys Gly Asn Thr Val Asn Gly Lys Ile Tyr Ala Val Pro
 115 120 125
 Val Ala Ala Asn Val Ala Ser Ser Gln Asn Phe Ala Phe Asn Gly Thr
 130 135 140
 Leu Leu Ala Lys Tyr Gly Ile Asp Ile Ser Gly Val Thr Ser Tyr Glu
 145 150 155 160
 Thr Leu Glu Pro Val Leu Lys Gln Ile Lys Glu Lys Ala Pro Asp Val
 165 170 175
 Val Pro Phe Ala Ile Gly Lys Val Phe Ile Pro Ser Asp Asn Phe Asp
 180 185 190
 Tyr Pro Val Ala Asn Gly Leu Pro Phe Val Ile Asp Leu Glu Gly Asp
 195 200 205
 Thr Thr Lys Val Val Asn Arg Tyr Glu Val Pro Arg Phe Lys Glu His
 210 215 220
 Leu Lys Thr Leu His Lys Phe Tyr Glu Ala Gly Tyr Ile Pro Lys Asp
 225 230 235 240
 Val Ala Thr Ser Asp Thr Ser Phe Asp Leu Gln Gln Asp Thr Trp Phe
 245 250 255
 Val Arg Glu Glu Thr Val Gly Pro Ala Asp Tyr Gly Asn Ser Leu Leu
 260 265 270
 Ser Arg Val Ala Asn Lys Asp Ile Gln Ile Lys Pro Ile Thr Asn Phe
 275 280 285
 Ile Lys Xaa Asn Gln Thr Thr Gln Val Ala Asn Phe Val Ile Ser Asn
 290 295 300
 Asn Ser Lys Asn Lys Glu Lys Ser Met Glu Ile Leu Asn Leu Leu Asn
 305 310 315 320
 Thr Asn Pro Glu Leu Leu Asn Gly Leu Val Tyr Gly Pro Glu Gly Lys

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325

330

335

Asn Trp Glu Lys Ile Glu Gly Lys Glu Asn Arg Val Arg Val Leu Asp
340 345 350

Gly Tyr Lys Gly Asn Thr His Met Gly Gly Trp Asn Thr Gly Asn Asn
355 360 365

Trp Ile Leu Tyr Ile Asn Glu Asn Val Thr Asp Gln Gln Ile Glu Asn
370 375 380

Ser Lys Lys Glu Leu Ala Glu Ala Lys Glu Ser Pro Ala Leu Gly Phe
385 390 395 400

Ile Phe Asn Thr Asp Asn Val Lys Ser Glu Ile Ser Ala Ile Ala Asn
405 410 415

Thr Met Gln Gln Phe Asp Thr Ala Ile Asn Thr Gly Thr Val Asp Pro
420 425 430

Asp Lys Ala Ile Pro Glu Leu Met Glu Lys Leu Lys Ser Glu Gly Ala
435 440 445

Tyr Glu Lys Val Leu Asn Glu Met Gln Lys Gln Tyr Asp Glu Phe Leu
450 455 460

Lys Asn Lys Lys
465

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 937 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

TGCTCAAGGA ACTGCTTCTA AAGACAACAA AGAGGCAGAA CTTAAGAAGG TTGACTTTAT	60
CCTAGACTGG ACACCAAATA CCAACCACAC AGGGCTTTAT GTTGCCAAGG AAAAAGGTTA	120
TTTCAAAGAA GCTGGAGTGG ATGTGTGATT GAAATIGCCA CCAGAAGAAA GTTCTTCTGA	180
CTTGGTTATC AACGGAAAGG CACCAFTTGC AGTGATTTC CAAGACTACA TGGCTAAGAA	240
ATTGGA AAAA GGAGCAGGAA TCACTGCCGT TGCAGCTATT GTTGAACACA ATACATCAGG	300
AATCATCTCT CGTAAATCTG ATAATGTAAG CAGTCCAAAA GACTTGGTTG GTAAGAAATA	360
TGGGACATGG AATGACCCAA CTGAACCTGC TATGTTGAAA ACCTTGGTAG AATCTCAAGG	420
TGGAGACTTT GAGAAGGTTG AAAAAGTACC AAATAACGAC TCAAAC TCAA TCACACCGAT	480
TGCCAATGGC GTCTTTGATA CTGCTTGGAT TTACTACGGT TGGGATGGTA TCCTTGCTAA	540
ATCTCAAGGT GTAGATGCTA ACTTCATGTA CTTGAAAGAC TATGTCAAGG AGTTTGACTA	600
CTATTACCA GTTATCATCG CAAACAACGA CTATCTGAAA GATAACAAG AAGAAGCTCG	660
CAAAGTCATC CAAGCCATCA AAAAAGGCTA CCAATATGCC ATGGAACATC CAGAAGAAGC	720

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TGCAGATATT CTCATCAAGA ATGCACCTGA ACTCAAGGAA AAACGTGACT TTGTCATCGA 780
 ATCTCAAAAA TACTTTGTCAA AAGAATACGC AAGCGACAAG GAAAAATGGG GTCAATTTGA 840
 CGCAGCTCGC TGGAAATGCTT TCTACAAATG GGATAAAGAA AATGGTATCC TTAAAGAAGA 900
 CTTGACAGAC AAAGGCTTCA CCAACGAATT TGTGAAA 937

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Gly Gln Gly Thr Ala Ser Lys Asp Asn Lys Glu Ala Glu Leu Lys Lys
 1 5 10 15
 Val Asp Phe Ile Leu Asp Trp Thr Pro Asn Thr Asn His Thr Gly Leu
 20 25 30
 Tyr Val Ala Lys Glu Lys Gly Tyr Phe Lys Glu Ala Gly Val Asp Val
 35 40 45
 Asp Leu Lys Leu Pro Pro Glu Glu Ser Ser Ser Asp Leu Val Ile Asn
 50 55 60
 Gly Lys Ala Pro Phe Ala Val Tyr Phe Gln Asp Tyr Met Ala Lys Lys
 65 70 75 80
 Leu Glu Lys Gly Ala Gly Ile Thr Ala Val Ala Ala Ile Val Glu His
 85 90 95
 Asn Thr Ser Gly Ile Ile Ser Arg Lys Ser Asp Asn Val Ser Ser Pro
 100 105 110
 Lys Asp Leu Val Gly Lys Lys Tyr Gly Thr Trp Asn Asp Pro Thr Glu
 115 120 125
 Leu Ala Met Leu Lys Thr Leu Val Glu Ser Gln Gly Gly Asp Phe Glu
 130 135 140
 Lys Val Glu Lys Val Pro Asn Asn Asp Ser Asn Ser Ile Thr Pro Ile
 145 150 155 160
 Ala Asn Gly Val Phe Asp Thr Ala Trp Ile Tyr Tyr Gly Trp Asp Gly
 165 170 175
 Ile Leu Ala Lys Ser Gln Gly Val Asp Ala Asn Phe Met Tyr Leu Lys
 180 185 190
 Asp Tyr Val Lys Glu Phe Asp Tyr Tyr Ser Pro Val Ile Ile Ala Asn
 195 200 205
 Asn Asp Tyr Leu Lys Asp Asn Lys Glu Glu Ala Arg Lys Val Ile Gln
 210 215 220

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Ala Ile Lys Lys Gly Tyr Gln Tyr Ala Met Glu His Pro Glu Glu Ala
 225 230 235 240

Ala Asp Ile Leu Ile Lys Asn Ala Pro Glu Leu Lys Glu Lys Arg Asp
 245 250 255

Phe Val Ile Glu Ser Gln Lys Tyr Leu Ser Lys Glu Tyr Ala Ser Asp
 260 265 270

Lys Glu Lys Trp Gly Gln Phe Asp Ala Ala Arg Trp Asn Ala Phe Tyr
 275 280 285

Lys Trp Asp Lys Glu Asn Gly Ile Leu Lys Glu Asp Leu Thr Asp Lys
 290 295 300

Gly Phe Thr Asn Glu Phe Val Lys
 305 310

(2) INFORMATION FOR SEQ ID NO: 13:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 799 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

TAGCTCAGGT GGAAACGCTG GTTCATCCTC TGGAAAAACA ACTGCCAAG CTCGCACTAT	60
CGATGAAATC AAAAAAGCG GTGAAGTGGC AATCGCCGTG TTGGAGATA AAAAACCGTT	120
TGGCTACGTT GACAATGATG GTTCTACCAA GGTACGCTAC GATATTGAAC TAGGGAACCA	180
ACTAGCTCAA GACCTTGGTG TCAAGGTTAA ATACATTTC A GTCGATGCTG CCAACCGTGC	240
GGAATACTTG ATTTCAAACA AGGTAGATAT TACTCTTGCT AACTTTACAG TAACTGACGA	300
ACGTAAGAAA CAAGTTGATT TTGCCCTTCC ATATATGAAA GTTCTCTG GGTGCTGATC	360
ACCTAAGACT GGTCTCATT CAGACGTCAA ACAACTTGAA GGTAAGACCT TAATTGTCAC	420
AAAAGGA 3 ACTGCTGAGA CTTATTTTGA AAAGAATCAT CCAGAAATCA AACTCCAAAA	480
ATACGACCAA TACAGTACT CTTACCAAGC TCTTCTTGAC GGACGTGGAG ATGCTTTTTC	540
AACTGACAA TCGGAAGTTC TAGCTTGGGC GCTTGAAAAA AAAGGATTG AAGTAGGAAT	600
TACTTCCCCT GGTGATCCCG ATACCATTGC GGCAGCAGTT CAAAAAGGCA ACCAAGAATT	660
GCTAGACTTC ATCAATAAAG ATATTGAAAA ATTAGGCAAG GAAAACCTCT TCCACAAGGC	720
CTATGAAAAA ACACTTCACC CAACCTACGG TGACGCTGCT AAAGCAGATG ACCTGGTTGT	780
TGAAGGTGGA AAAGTTGAT	799

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 266 amino acids
 (B) TYPE: amino acid

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(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Ser Ser Gly Gly Asn Ala Gly Ser Ser Ser Gly Lys Thr Thr Ala Lys
 1 5 10 15
 Ala Arg Thr Ile Asp Glu Ile Lys Lys Ser Gly Glu Leu Arg Ile Ala
 20 25 30
 Val Phe Gly Asp Lys Lys Pro Phe Gly Tyr Val Asp Asn Asp Gly Ser
 35 40 45
 Thr Lys Val Arg Tyr Asp Ile Glu Leu Gly Asn Gln Leu Ala Gln Asp
 50 55 60
 Leu Gly Val Lys Val Lys Tyr Ile Ser Val Asp Ala Ala Asn Arg Ala
 65 70 75 80
 Glu Tyr Leu Ile Ser Asn Lys Val Asp Ile Thr Leu Ala Asn Phe Thr
 85 90 95
 Val Thr Asp Glu Arg Lys Lys Gln Val Asp Phe Ala Leu Pro Tyr Met
 100 105 110
 Lys Val Ser Leu Gly Val Val Ser Pro Lys Thr Gly Leu Ile Thr Asp
 115 120 125
 Val Lys Gln Leu Glu Gly Lys Thr Leu Ile Val Thr Lys Gly Thr Thr
 130 135 140
 Ala Glu Thr Tyr Phe Glu Lys Asn His Pro Glu Ile Lys Leu Gln Lys
 145 150 155 160
 Tyr Asp Gln Tyr Ser Asp Ser Tyr Gln Ala Leu Leu Asp Gly Arg Gly
 165 170 175
 Asp Ala Phe Ser Thr Asp Asn Thr Glu Val Leu Ala Trp Ala Leu Glu
 180 185 190
 Asn Lys Gly Phe Glu Val Gly Ile Thr Ser Leu Gly Asp Pro Asp Thr
 195 200 205
 Ile Ala Ala Ala Val Gln Lys Gly Asn Gln Glu Leu Leu Asp Phe Ile
 210 215 220
 Asn Lys Asp Ile Glu Lys Leu Gly Lys Glu Asn Phe Phe His Lys Ala
 225 230 235 240
 Tyr Glu Lys Thr Leu His Pro Thr Tyr Gly Asp Ala Ala Lys Ala Asp
 245 250 255
 Asp Leu Val Val Glu Gly Gly Lys Val Asp
 260 265

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1189 base pairs

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(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

CTCCAACTAT GGTAAATCTG CGGATGGCAC AGTGACCATC GAGTATTCA ACCAGAAAAA	60
AGAAATGACC AAAACCTTGG AAGAAATCAC TCGTGATTTT GAGAAGGAAA ACCCTAAGAT	120
CAAGGTCAA GTCGTCATG TACCAAATGC TGGTGAAGTA TTGAAGACAC GCCTTCTCGC	180
AGGAGATGTG CCTGATGTGG TCAATATTTA CCCACAGTCC ATCGAACTGC AAGAATGGGC	240
AAAAGCAGGT GTTTTTGAAG ATTTGAGCAA CAAAGACTAC CTGAAACGCG TGAAAAATGG	300
CTACGCTGAA AAATATGCTG TAAACGAAAA AGTTTACAAC GTTCCTTTTA CAGCTAATGC	360
TTATGGAATT TACTACAACA AAGATAAATT CGAAGAAGTC GGCTTGAAGG TTCCTGAAAC	420
CTGGGATGAA TTTGAACAGT TAGTCAAAGA TATCGTTGCT AAGGACAAA CACCATTTGG	480
AATTGCAGGT GCAGATGCTT GGACACTCAA TGGTTACAAT CAATTAGCCT TTGCACAGC	540
AACAGTGGGA GGAAAAGAAG CAAATCAATA CCTTCGTTAT TCTCAACCAA ATGCCATTAA	600
ATTGTCCGAT CCGATTATGA AAGATGATAT CAAGGTCATG GACATCCTTC GCATCAATGG	660
ATCTAAGCAA AAGAACTGGG AAGGTGCTGG CTATACCGAT GTTATCGGAG CCTTCGCACG	720
TGGGGATGTC CTCATGACAC CAAATGGGTC TTGGGCGATC ACAGCGATTA ATGAACAAAA	780
ACCGAACTTT AAGATTGGGA CCTTCATGAT TCCAGGAAAA GAAAAGGAC AAAGCTTAAC	840
CGTGTGTGCG GGAGACTTGG CATGGTCTAT CTCAGCCACC ACCAAACATC CAAAAGAAGC	900
CAATGCCTTT GTGGAATATA TGACCCGTCC AGAAGTCATG CAAAATACT ACGATGTGGA	960
CGGATCTCCA ACAGCGATCG AAGGGGTCAA ACAAGCAGGA GAAGATTAC CGCTTGCTGG	1020
TATGACCGAA TATGCTTTA CGGATCGTCA CTTGGTCTGG TTGCAACAAT ACTGGACCAG	1080
TGAAGCAGAC TTCCATACCT TGACCATGAA CTATGTCTTG ACCGGTGATA AACAAGGCAT	1140
GGTCAATGAT TTGAATGCC TCTTTAATCC GATGAAAGCG GATGTGGAT	1189

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 396 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Ser	Asn	Tyr	Gly	Lys	Ser	Ala	Asp	Gly	Thr	Val	Thr	Ile	Glu	Tyr	Phe
1				5					10					15	

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Asn Gln Lys Lys Glu Met Thr Lys Thr Leu Glu Glu Ile Thr Arg Asp
 20 25 30
 Phe Glu Lys Glu Asn Pro Lys Ile Lys Val Lys Val Val Asn Val Pro
 35 40 45
 Asn Ala Gly Glu Val Leu Lys Thr Arg Val Leu Ala Gly Asp Val Pro
 50 55 60
 Asp Val Val Asn Ile Tyr Pro Gln Ser Ile Glu Leu Gln Glu Trp Ala
 65 70 75 80
 Lys Ala Gly Val Phe Glu Asp Leu Ser Asn Lys Asp Tyr Leu Lys Arg
 85 90 95
 Val Lys Asn Gly Tyr Ala Glu Lys Tyr Ala Val Asn Glu Lys Val Tyr
 100 105 110
 Asn Val Pro Phe Thr Ala Asn Ala Tyr Gly Ile Tyr Tyr Asn Lys Asp
 115 120 125
 Lys Phe Glu Glu Leu Gly Leu Lys Val Pro Glu Thr Trp Asp Glu Phe
 130 135 140
 Glu Gln Leu Val Lys Asp Ile Val Ala Lys Gly Gln Thr Pro Phe Gly
 145 150 155 160
 Ile Ala Gly Ala Asp Ala Trp Thr Leu Asn Gly Tyr Asn Gln Leu Ala
 165 170 175
 Phe Ala Thr Ala Thr Gly Gly Gly Lys Glu Ala Asn Gln Tyr Leu Arg
 180 185 190
 Tyr Ser Gln Pro Asn Ala Ile Lys Leu Ser Asp Pro Ile Met Lys Asp
 195 200 205
 Asp Ile Lys Val Met Asp Ile Leu Arg Ile Asn Gly Ser Lys Gln Lys
 210 215 220
 Asn Trp Glu Gly Ala Gly Tyr Thr Asp Val Ile Gly Ala Phe Ala Arg
 225 230 235 240
 Gly Asp Val Leu Met Thr Pro Asn Gly Ser Trp Ala Ile Thr Ala Ile
 245 250 255
 Asn Glu Gln Lys Pro Asn Phe Lys Ile Gly Thr Phe Met Ile Pro Gly
 260 265 270
 Lys Glu Lys Gly Gln Ser Leu Thr Val Gly Ala Gly Asp Leu Ala Trp
 275 280 285
 Ser Ile Ser Ala Thr Thr Lys His Pro Lys Glu Ala Asn Ala Phe Val
 290 295 300
 Glu Tyr Met Thr Arg Pro Glu Val Met Gln Lys Tyr Tyr Asp Val Asp
 305 310 315 320
 Gly Ser Pro Thr Ala Ile Glu Gly Val Lys Gln Ala Gly Glu Asp Ser
 325 330 335
 Pro Leu Ala Gly Met Thr Glu Tyr Ala Phe Thr Asp Arg His Leu Val
 340 345 350

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Trp Leu Gln Gln Tyr Trp Thr Ser Glu Ala Asp Phe His Thr Leu Thr
355 360 365

Met Asn Tyr Val Leu Thr Gly Asp Lys Gln Gly Met Val Asn Asp Leu
370 375 380

Asn Ala Phe Phe Asn Pro Met Lys Ala Asp Val Asp
385 390 395

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 775 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

TGGGAAAAAT TCTAGCGAAA CTAGTGGAGA TAATTGGTCA AAGTACCAGT CTAACAAGTC	60
TATTACTATT GGATTTGATA GTACTTTTGT TCCAATGGGA TTGCTCAGA AAGATGGTTC	120
TTATGCAGGA TTTGATATTG ATTTAGCTAC AGCTGTTTTT GAAAAATACG GAATCACGGT	180
AAATTGGCAA CCGATTGATT GGGATTTGAA AGAAGCTGAA TTGACAAAAG GAACGATTGA	240
TCTGATTGG AATGGCTATT CCGCTACAGA CGAACGCCGT GAAAAGGTGG CTTTCAGTAA	300
CTCATATATG AAGAATGAGC AGGTATTGGT TACGAAGAAA TCATCTGSTA TCACGACTGC	360
AAAGGATATG ACTGGAAGA CATTAGGAGC TCAAGCTGGT TCATCTGGTT ATGCGGACTT	420
TGAAGCAAA CCAGAAATTT TGAAGAATAT TGTGCGTAAT AAGGAAGCGA ATCAATACCA	480
AACCTTTAAT GAAGCCTTGA TTGATTTGAA AAACGATCGA ATTGATGGTC TATTGATTGA	540
CCGTGTCTAT GCAAACCTATT ATTTAGAAGC AGAAGGTGTT TTAACGATT ATAATGTCCTT	600
TACAGTTGGA CTAGAAACAG AAGCTTTTGC GGTGGAGGCC CGTAAGGAAG ATACAAACTT	660
GGTTAAGGAG ATAAATGAAG CTTTTCCTAG TCTTTACAAG GACGGCAAGT TCCAAGAAAT	720
CAGCCAAAAA TGGTTTGGAG AAGATGTAGC AACCAAAGAA GTAAAAGAAG GACAG	775

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Gly Lys Asn Ser Ser Glu Thr Ser Gly Asp Asn Trp Ser Lys Tyr Gln
1 5 10 15	
Ser Asn Lys Ser Ile Thr Ile Gly Phe Asp Ser Thr Phe Val Pro Met	

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20	25	30
Gly Phe Ala Gln Lys Asp Gly Ser Tyr Ala Gly Phe Asp Ile Asp Leu 35 40 45		
Ala Thr Ala Val Phe Glu Lys Tyr Gly Ile Thr Val Asn Trp Gln Pro 50 55 60		
Ile Asp Trp Asp Leu Lys Glu Ala Glu Leu Thr Lys Gly Thr Ile Asp 65 70 75 80		
Leu Ile Trp Asn Gly Tyr Ser Ala Thr Asp Glu Arg Arg Glu Lys Val 85 90 95		
Ala Phe Ser Asn Ser Tyr Met Lys Asn Glu Gln Val Leu Val Thr Lys 100 105 110		
Lys Ser Ser Gly Ile Thr Thr Ala Lys Asp Met Thr Gly Lys Thr Leu 115 120 125		
Gly Ala Gln Ala Gly Ser Ser Gly Tyr Ala Asp Phe Glu Ala Asn Pro 130 135 140		
Glu Ile Leu Lys Asn Ile Val Ala Asn Lys Glu Ala Asn Gln Tyr Gln 145 150 155 160		
Thr Phe Asn Glu Ala Leu Ile Asp Leu Lys Asn Asp Arg Ile Asp Gly 165 170 175		
Leu Leu Ile Asp Arg Val Tyr Ala Asn Tyr Tyr Leu Glu Ala Glu Gly 180 185 190		
Val Leu Asn Asp Tyr Asn Val Phe Thr Val Gly Leu Glu Thr Glu Ala 195 200 205		
Phe Ala Val Gly Ala Arg Lys Glu Asp Thr Asn Leu Val Lys Lys Ile 210 215 220		
Asn Glu Ala Phe Ser Ser Leu Tyr Lys Asp Gly Lys Phe Gln Glu Ile 225 230 235 240		
Ser Gln Lys Trp Phe Gly Glu Asp Val Ala Thr Lys Glu Val Lys Glu 245 250 255		
Gly Gln		

(2) INFORMATION FOR SEQ ID NO: 19:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 868 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

TCCTAGCGGA AAAAAGATA CAACTTCTGG TCAAAACTA AAAGTTGTTG CTACAAACTC	60
AATCATCGCT GATATTACTA AAAATATGTC TGGTGACAAA ATTGACCTTC ATAGTATCGT	120

TCCGATTGGG CAAGACCCAC ACGAATACGA ACCACTTCCT GAAGACGTTA AGAAAACTTC 180
 TGAGGCTAAT TTGATTTTCT ATAACGGTAT CAACCTTGAA ACAGGTGGCA ATGCTTGGTT 240
 TACAAAAATTG GTAGAAAAATG CCAAGAAAAC TGAAAACAAA GACTACTTCG CAGTCAGCGA 300
 CGCGCTTGAT GTTATCTACC TTGAAGGTCA AAATGAAAAA GGAAAAGAAG ACCCACACGC 360
 TTGGCTTAAC CTGTAAAAACG GTATTATTTT TGCTAAAAAT ATCGCCAAAC AATTGAGCGC 420
 CAAAGACCCCT AACAATAAAG AATTCTATGA AAAAAATCTC AAAGAATATA CTGATAAGTT 480
 AGACAAACTT GATAAAGAAA GTAAGGATAA ATTTAATAAG ATCCCTGCTG AAAAGAAACT 540
 CATTGTAACC AGCGAAGGAG CATTCAAATA CTTCCTTAAA GCCTATGGTG TCCCAAGTGC 600
 TTACATCTGG GAAATCAATA CTGAAGAAGA AGGAACTCCT GAACAAATCA AGACCTTGGT 660
 TGAAAAAATT CGCCAAACAA AAGTTCCATC ACTCTTTGTA GAATCAAGTG TGGATGACCG 720
 TCCAATGAAA ACTGTTTCTC AAGACACAAA CATCCCAATC TACGCTCAAA TCTTTACTGA 780
 CTCTATCGCA GAACAAGGTA AAGAAGGCGA CAGCTACTAC AGCATGATGA AATACAACCT 840
 TGACAAGATT GCTGAAGGAT TGGCAAAA 868

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 289 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Ala Ser Gly Lys Lys Asp Thr Thr Ser Gly Gln Lys Leu Lys Val Val
 1 5 10 15
 Ala Thr Asn Ser Ile Ile Ala Asp Ile Thr Lys Asn Ile Ala Gly Asp
 20 25 30
 Lys Ile Asp Leu His Ser Ile Val Pro Ile Gly Gln Asp Pro His Glu
 35 40 45
 Tyr Glu Pro Leu Pro Glu Asp Val Lys Lys Thr Ser Glu Ala Asn Leu
 50 55 60
 Ile Phe Tyr Asn Gly Ile Asn Leu Glu Thr Gly Gly Asn Ala Trp Phe
 65 70 75 80
 Thr Lys Leu Val Glu Asn Ala Lys Lys Thr Glu Asn Lys Asp Tyr Phe
 85 90 95
 Ala Val Ser Asp Gly Val Asp Val Ile Tyr Leu Glu Gly Gln Asn Glu
 100 105 110
 Lys Gly Lys Glu Asp Pro His Ala Trp Leu Asn Leu Glu Asn Gly Ile
 115 120 125

Ile Phe Ala Lys Asn Ile Ala Lys Gln Leu Ser Ala Lys Asp Pro Asn
 130 135 140
 Asn Lys Glu Phe Tyr Glu Lys Asn Leu Lys Glu Tyr Thr Asp Lys Leu
 145 150 155 160
 Asp Lys Leu Asp Lys Glu Ser Lys Asp Lys Phe Asn Lys Ile Pro Ala
 165 170 175
 Glu Lys Lys Leu Ile Val Thr Ser Glu Gly Ala Phe Lys Tyr Phe Ser
 180 185 190
 Lys Ala Tyr Gly Val Pro Ser Ala Tyr Ile Trp Glu Ile Asn Thr Glu
 195 200 205
 Glu Glu Gly Thr Pro Glu Gln Ile Lys Thr Leu Val Glu Lys Leu Arg
 210 215 220
 Gln Thr Lys Val Pro Ser Leu Phe Val Glu Ser Ser Val Asp Asp Arg
 225 230 235 240
 Pro Met Lys Thr Val Ser Gln Asp Thr Asn Ile Pro Ile Tyr Ala Gln
 245 250 255
 Ile Phe Thr Asp Ser Ile Ala Glu Gln Gly Lys Glu Gly Asp Ser Tyr
 260 265 270
 Tyr Ser Met Met Lys Tyr Asn Leu Asp Lys Ile Ala Glu Gly Leu Ala
 275 280 285
 Lys

(2) INFORMATION FOR SEQ ID NO: 21:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1546 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

TGGCTCAAAA AATACAGCTT CAAGTCCAGA TTATAAGTTG GAAGGTGTAA CATTCGCGCT	60
TCAAGAAAAA AAAACATTGA AGTTTATGAC AGCCAGTTCA CCGTTATCTC CTAAGACCC	120
AAATGAAAAA TTAATTTTGC AACGTTTGGA GAAGGAAACT GCGGTCATA TTGACTGGAC	180
CAACTACCAA TCCGACTTTG CAGAAAAACG TAACCTGGAT ATTCTAGTG GTGATTTACC	240
AGATGCTATC CACAACGACG GAGCTTCAGA TGTGGACTTG ATGAAGTGGG CTAAGAAAGG	300
TGTTATTATT CCAGTTGAAG ATTTGATTGA TAAATACATG CCAAAATCTTA AGAAAATTTT	360
GGATGAGAAA CCAGAGTACA AGGCCTTGAT GACAGCACCT GATGGGCACA TTACTCATT	420
TCCATGGATT GAAGAGCTTG GAGATGGTAA AGAGTCTATT CACAGTGTC ACGATATGGC	480
TTGGATTAAAC AAAGATTGGC TTAAGAAACT TGGTCTTGAA ATGCCAAAAA CTACTGATGA	540

TTTGATTAAA GTCCTAGAAG CTTTCAAAAA CGGGGATCCA AATGGAAATG GAGAGGCTGA 600
 TGAATTTCCA TTTTCATTTA TTAGTGGTAA CGGAAACGAA GATTTTAAAT TCCTATTTCG 660
 TGCATTTTGGT ATAGGGGATA ACGATGATCA TTAGTAGTA GGAATGATG GCAAAGTTGA 720
 CTTTCACAGCA GATAACGATA ACTATAAAGA AGSTGTCAA TTTATCCGTC AATTGCAAGA 780
 AAAAGGCCTG ATTGATAAAG AAGCTTTCGA ACATGATTGG AATAGTTACA TGTCTAAAGG 840
 TCATGATCAG AAATTTGGTG TTTACTTTAC ATGGGATAAG AATAATGTTA CTGGAAGTAA 900
 CGAAAGTTAT GATGTTTTAC CAGTACTTGC TGGACCAAGT GGTCAAAAAC ACGTAGCTCG 960
 TACAAACGGT ATGGGATTTC CACGTGACAA GATGGTTATT ACCAGTGTA AAAAAACCT 1020
 AGAATTGACA GCTAAATGGA TTGATGCACA ATACGCTCCA CTCCAATCTG TGCAAAATAA 1080
 CTGGGGAAC TACGAGATG ACAACAACA AAACATCTTT GAATTGGATC AAGCGTCAAA 1140
 TAGTCTAAAA CACTTACCAC TAAACGGAAC TGCACCAGCA GAACCTCGTC AAAAGACTGA 1200
 AGTAGGAGGA CCACTAGCTA TCCTAGATTC ATACTATGGT AAAGTAACAA CCATGCGCTGA 1260
 TGATGCCAAA TGGCGTTTGG ATCTTATCAA AGAATATTAT GTTCCTTACA TGAGCAATGT 1320
 CAATAACTAT CCAAGAGTCT TTATGACACA GGAAGATTTC GACAAGATTG CCCATATCGA 1380
 AGCAGATATG AATGACTATA TCTACCGTAA ACGTGCTGAA TGGATTGTAA ATGGCAATAT 1440
 TGATACTGAG TGGGATGATT ACAAGAAAGA ACTTGAAAA TACGGACTTT CTGATTACCT 1500
 CGCTATTAAA CAAAAFACT ACGACCAATA CCAAGCAAAC AAAAAC 1546

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 515 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Gly Ser Lys Asn Thr Ala Ser Ser Pro Asp Tyr Lys Leu Glu Gly Val
 1 5 10 15
 Thr Phe Pro Leu Gln Glu Lys Lys Thr Leu Lys Phe Met Thr Ala Ser
 20 25 30
 Ser Pro Leu Ser Pro Lys Asp Pro Asn Glu Lys Leu Ile Leu Gln Arg
 35 40 45
 Leu Glu Lys Glu Thr Gly Val His Ile Asp Trp Thr Asn Tyr Gln Ser
 50 55 60
 Asp Phe Ala Glu Lys Arg Asn Leu Asp Ile Ser Ser Gly Asp Leu Pro
 65 70 75 80
 Asp Ala Ile His Asn Asp Gly Ala Ser Asp Val Asp Leu Met Asn Trp

Ala Lys Lys Gly Val Ile Ile Pro Val Glu Asp Leu Ile Asp Lys Tyr
100 105 110

Met Pro Asn Leu Lys Lys Ile Leu Asp Glu Lys Pro Glu Tyr Lys Ala
115 120 125

Leu Met Thr Ala Pro Asp Gly His Ile Tyr Ser Phe Pro Trp Ile Glu
130 135 140

Glu Leu Gly Asp Gly Lys Glu Ser Ile His Ser Val Asn Asp Met Ala
145 150 155 160

Trp Ile Asn Lys Asp Trp Leu Lys Lys Leu Gly Leu Glu Met Pro Lys
165 170 175

Thr Thr Asp Asp Leu Ile Lys Val Leu Glu Ala Phe Lys Asn Gly Asp
180 185 190

Pro Asn Gly Asn Gly Glu Ala Asp Glu Ile Pro Phe Ser Phe Ile Ser
195 200 205

Gly Asn Gly Asn Glu Asp Phe Lys Phe Leu Phe Ala Ala Phe Gly Ile
210 215 220

Gly Asp Asn Asp Asp His Leu Val Val Gly Asn Asp Gly Lys Val Asp
225 230 235 240

Phe Thr Ala Asp Asn Asp Asn Tyr Lys Glu Gly Val Lys Phe Ile Arg
245 250 255

Gln Leu Gln Glu Lys Gly Leu Ile Asp Lys Glu Ala Phe Glu His Asp
260 265 270

Trp Asn Ser Tyr Ile Ala Lys Gly His Asp Gln Lys Phe Gly Val Tyr
275 280 285

Phe Thr Trp Asp Lys Asn Asn Val Thr Gly Ser Asn Glu Ser Tyr Asp
290 295 300

Val Leu Pro Val Leu Ala Gly Pro Ser Gly Gln Lys His Val Ala Arg
305 310 315 320

Thr Asn Gly Met Gly Phe Ala Arg Asp Lys Met Val Ile Thr Ser Val
325 330 335

Asn Lys Asn Leu Glu Leu Thr Ala Lys Trp Ile Asp Ala Gln Tyr Ala
340 345 350

Pro Leu Gln Ser Val Gln Asn Asn Trp Gly Thr Tyr Gly Asp Asp Lys
355 360 365

Gln Gln Asn Ile Phe Glu Leu Asp Gln Ala Ser Asn Ser Leu Lys His
370 375 380

Leu Pro Leu Asn Gly Thr Ala Pro Ala Glu Leu Arg Gln Lys Thr Glu
385 390 395 400

Val Gly Gly Pro Leu Ala Ile Leu Asp Ser Tyr Tyr Gly Lys Val Thr
405 410 415

Thr Met Pro Asp Asp Ala Lys Trp Arg Leu Asp Leu Ile Lys Glu Tyr

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136

420

425

430

Tyr Val Pro Tyr Met Ser Asn Val Asn Asn Tyr Pro Arg Val Phe Met
 435 440 445
 Thr Gln Glu Asp Leu Asp Lys Ile Ala His Ile Glu Ala Asp Met Asn
 450 455 460
 Asp Tyr Ile Tyr Arg Lys Arg Ala Glu Trp Ile Val Asn Gly Asn Ile
 465 470 475 480
 Asp Thr Glu Trp Asp Asp Tyr Lys Lys Glu Leu Glu Lys Tyr Gly Leu
 485 490 495
 Ser Asp Tyr Leu Ala Ile Lys Gln Lys Tyr Tyr Asp Gln Tyr Gln Ala
 500 505 510
 Asn Lys Asn
 515

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 895 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

TAGTACAAAC TCAAGCTACT GTCAGACAGA GACCACTAGC TCTGCTCCAA CAGAGGTAAC 60
 CATTAAGT TCACTGGACG AGGTCAAAC TTCCAAAGT CTGAAAAGA TTGTGACCTT 120
 TGACCTCGGC GCTGCGGATA CTTATTCGCGC TTTAGGATTT GAAAAAATA TCGTCGGAAT 180
 GCCTACAAAA ACTGTTCCGA CTTATCTAAA AGACCTAGTG GGAAGTGTCA AAAATGTTGG 240
 TTCTATGAAA GAACCTGATT TAGAAGCTAT CGCCGCCCTT GAGCCTGATT TGATTATCGC 300
 TTCGCCACGT ACACAAAAT TCGTAGACAA ATTCAAAGAA ATCGCCCAA CCGTTCTCTT 360
 CCAAGCAAGC AAGGACGACT ACTGGACTTC TACCAAGGCT AATATCGAAT CCTTAGCAAG 420
 TGCCTTCGCG GAACTGGTA CACAGAAAGC CAAGGAAGAA TTGACCAAGC TAGACAAGAG 480
 CATCCAAGAA GTCCTACTA AAAATGAAAG CTCTGACAAA AAGCCCTTG CGATCCTCCT 540
 TAATGAAGGA AAAATGGCAG CCTTTGGTGC CAAATCTCGT TTCTCTTTCT TGTACCAAAC 600
 CTTGAAATTC AAACCAACTG ATACAAAATT TGAAGACTCA CGCCACGGAC AAGAAGTCAG 660
 CTTTGAAAGT GTCAAAGAAA TCAACCTGTA CATCCTCTTT GTCATCAACC GTACCCCTTGC 720
 CATCGGTGGG GACAACCTTA GCAACGACGG TGTCTAGAA AATGCCCTTA TCGCTGAAAC 780
 ACCTGTGCTT AAAATGGTA AGATTATCCA ACTAACACCA GACCTCTGGT ATCTAAGCGG 840
 AGGCGGACTT GAATCAACAA AACTCATGAT TGAAGACATA CAAAAGCTT TGAAA 895

(2) INFORMATION FOR SEQ ID NO:24:

102627.04201

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 298 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

```

Ser Thr Asn Ser Ser Thr Ser Gln Thr Glu Thr Ser Ser Ser Ala Pro
1      5      10      15

Thr Glu Val Thr Ile Lys Ser Ser Leu Asp Glu Val Lys Leu Ser Lys
20      25      30

Val Pro Glu Lys Ile Val Thr Phe Asp Leu Gly Ala Ala Asp Thr Ile
35      40      45

Arg Ala Leu Gly Phe Glu Lys Asn Ile Val Gly Met Pro Thr Lys Thr
50      55      60

Val Pro Thr Tyr Leu Lys Asp Leu Val Gly Thr Val Lys Asn Val Gly
65      70      75      80

Ser Met Lys Glu Pro Asp Leu Glu Ala Ile Ala Ala Leu Glu Pro Asp
85      90      95

Leu Ile Ile Ala Ser Pro Arg Thr Gln Lys Phe Val Asp Lys Phe Lys
100     105     110

Glu Ile Ala Pro Thr Val Leu Phe Gln Ala Ser Lys Asp Asp Tyr Trp
115     120     125

Thr Ser Thr Lys Ala Asn Ile Glu Ser Leu Ala Ser Ala Phe Gly Glu
130     135     140

Thr Gly Thr Gln Lys Ala Lys Glu Glu Leu Thr Lys Leu Asp Lys Ser
145     150     155     160

Ile Gln Glu Val Ala Thr Lys Asn Glu Ser Ser Asp Lys Lys Ala Leu
165     170     175

Ala Ile Leu Leu Asn Glu Gly Lys Met Ala Ala Phe Gly Ala Lys Ser
180     185     190

Arg Phe Ser Phe Leu Tyr Gln Thr Leu Lys Phe Lys Pro Thr Asp Thr
195     200     205

Lys Phe Glu Asp Ser Arg His Gly Gln Glu Val Ser Phe Glu Ser Val
210     215     220

Lys Glu Ile Asn Pro Asp Ile Leu Phe Val Ile Asn Arg Thr Leu Ala
225     230     235     240

Ile Gly Gly Asp Asn Ser Ser Asn Asp Gly Val Leu Glu Asn Ala Leu
245     250     255

Ile Ala Glu Thr Pro Ala Ala Lys Asn Gly Lys Ile Ile Gln Leu Thr
260     265     270

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Pro Asp Leu Trp Tyr Leu Ser Gly Gly Gly Leu Glu Ser Thr Lys Leu
275 280 285

Met Ile Glu Asp Ile Gln Lys Ala Leu Lys
290 295

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1261 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

TGGCAATTCT GCGGAAGTA AAGATGCTGC CAAATCAGGT GGTGACGGTG CCAAAACAGA	60
AATCACTTGG TGGGCATTCC CAGTATTTAC CCAAGAAAAA ACTGGTGACG GTGTTGGAAC	120
TTATGAAAAA TCAATCATCG AAGCGTTTGA AAAAGCAAAAC CCAGATATAA AAGTGAAATT	180
GGAAACCATC GACTTCAAGT CAGGTCTCTGA AAAAATCACA ACAGCCATCG AAGCAGGAAC	240
AGCTCCAGAC GTACTCTTTG ATGCACCAGG ACGTATCATC CAATACGGTA AAAACGGTAA	300
ATTGGCTGAG TTGAATGACC TCTTCACAGA TGAATTTGTT AAAGATGTCA ACAATGAAAA	360
CATCGTACAA GCAAGTAAG CTGGAGACAA GGCTTATATG TATCCGATTA GTTCTGCCCC	420
ATTCTACATG GCAATGAACA AGAAAAATGTT AGAAGATGCT GGAGTAGCAA ACCTTGTAAG	480
AGAAGGTTGG ACAACTGATG ATTTTGAAAA AGTATTGAAA GCACTTAAAG ACAAGGGTTA	540
CACACCAGGT TCATTGTTCA GTTCTGGTCA AGGGGGAGAC CAAGGAACAC GTGCCTTTAT	600
CTCTAACCTT TATAGCGGTT CTGTAACAGA TGA AAAAAGTT AGCAAATATA CAACTGATGA	660
TCCTAAATTC GTCAAAGTTC TTGAAAAAGC AACTAGCTGG ATTAAAGACA ATTTGATCAA	720
TAATGGTTCA CAATTTGACG GTGGGGCAGA TATCCAAAAC TTGCCAACG GTCAAACATC	780
TTACACAATC CTTTGGGCAC CAGCTCAAAA TGGTATCCAA GCTAAACTTT TAGAAGCAAG	840
TAAGGTAGAA GTGGTAGAAG TACCATTCCC ATCAGACGAA GGTAGCCAG CTCCTGAGTA	900
CCTTGTAAC GGGTTTGACG TATTCAACAA TAAAGACGAC AAGAAAGTCG CTGCATCTAA	960
GAAATTCATC CAGTTTATCG CAGATGACAA GGAGTGGGGA CCTAAAGACG TAGTTCGTAC	1020
AGGTGCTTTC CCAGTCCGTA CTTCAATTGG AAAACTTTAT GAAGACAAAC GCATGGAAC	1080
AATCAGCGCG TGGACTCAAT ACTACTCACC ATACTACAAC ACTATTGATG GATTTCGTGA	1140
AATGAGAACA CTTTGGTTCC CAATGTTGCA ATCTGTATCA AATGGTGACG AAAAACCCAGC	1200
AGATGCTTTG AAAGCCTTCA CTGAAAAAGC GAACGAAACA ATCAAAAAG CTATGAAACA	1260

A

1261

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 420 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

```

Gly Asn Ser Gly Gly Ser Lys Asp Ala Ala Lys Ser Gly Gly Asp Gly
 1             5             10             15

Ala Lys Thr Glu Ile Thr Trp Trp Ala Phe Pro Val Phe Thr Gln Glu
 20             25             30

Lys Thr Gly Asp Gly Val Gly Thr Tyr Glu Lys Ser Ile Ile Glu Ala
 35             40             45

Phe Glu Lys Ala Asn Pro Asp Ile Lys Val Lys Leu Glu Thr Ile Asp
 50             55             60

Phe Lys Ser Gly Pro Glu Lys Ile Thr Thr Ala Ile Glu Ala Gly Thr
 65             70             75             80

Ala Pro Asp Val Leu Phe Asp Ala Pro Gly Arg Ile Ile Gln Tyr Gly
 85             90             95

Lys Asn Gly Lys Leu Ala Glu Leu Asn Asp Leu Phe Thr Asp Glu Phe
100             105             110

Val Lys Asp Val Asn Asn Glu Asn Ile Val Gln Ala Ser Lys Ala Gly
115             120             125

Asp Lys Ala Tyr Met Tyr Pro Ile Ser Ser Ala Pro Phe Tyr Met Ala
130             135             140

Met Asn Lys Lys Met Leu Glu Asp Ala Gly Val Ala Asn Leu Val Lys
145             150             155             160

Glu Gly Trp Thr Thr Asp Asp Phe Glu Lys Val Leu Lys Ala Leu Lys
165             170             175

Asp Lys Gly Tyr Thr Pro Gly Ser Leu Phe Ser Ser Gly Gln Gly Gly
180             185             190

Asp Gln Gly Thr Arg Ala Phe Ile Ser Asn Leu Tyr Ser Gly Ser Val
195             200             205

Thr Asp Glu Lys Val Ser Lys Tyr Thr Thr Asp Asp Pro Lys Phe Val
210             215             220

Lys Gly Leu Glu Lys Ala Thr Ser Trp Ile Lys Asp Asn Leu Ile Asn
225             230             235             240

Asn Gly Ser Gln Phe Asp Gly Gly Ala Asp Ile Gln Asn Phe Ala Asn
245             250             255

Gly Gln Thr Ser Tyr Thr Ile Leu Trp Ala Pro Ala Gln Asn Gly Ile
260             265             270

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(2) INFORMATION FOR SEQ ID NO: 27:

(A) LENGTH: 658 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

TTCAACAAGAA	AAAACAAAA	ATGAAGATGG	AGAAACTAAG	ACAGAACAGA	CAGCCAAAGC	60
TGATGGAACA	GTCGGTAGTA	AGTCTCAAGG	AGCTGCCCAG	AAGAAAGCAG	AAGTGGTCAA	120
TAAAGGTGAT	TACTACAGCA	TTCAAGGGAA	ATACGATGAA	ATATCGTAG	CCAACAAACA	180
CTATCCATTG	TCTAAAGACT	ATAATCCAGG	GGAAAATCCA	ACAGCCAAGG	CAGAGTTGGT	240
CAAACCTATC	AAAGCGATGC	AAGAGGCAGG	TTTCCCTATT	AGTGATCATT	ACAGTGGTTT	300
TAGAAGTTAT	GAAACTCAGA	CCAAGCTCTA	TCAAGATTAT	GTCAACCAAG	ATGGAAAGGC	360
AGCAGCTGAC	CGTTACTCTG	CCCGTCCTGG	CTATAGCGAA	CACCAGACAG	GCTTGGCCTT	420
TGATGTGATT	GGGACTGATG	GTGATTTGGT	GACAGAAGAA	AAAGCAGCCC	AATGGCTCTT	480
GGATCATGCA	GCTGATTATG	GCTTGTGTGT	CCGTTATCTC	AAAGGCAAGG	AAAAGGAAAC	540
AGGCTATATG	GCTGAAGAAT	GGCACCTGCG	TTATGTAGGA	AAAGAAGCTA	AAGAAATGCA	600
TGCAAGTGGT	CTCAGTTTGG	AAGAATACTA	TGGCTTTGAA	GGCGGAGACT	ACGTCGAT	658

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 219 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

```

Ser Gln Glu Lys Thr Lys Asn Glu Asp Gly Glu Thr Lys Thr Glu Gln
 1             5             10             15

Thr Ala Lys Ala Asp Gly Thr Val Gly Ser Lys Ser Gln Gly Ala Ala
      20             25             30

Gln Lys Lys Ala Glu Val Val Asn Lys Gly Asp Tyr Tyr Ser Ile Gln
      35             40             45

Gly Lys Tyr Asp Glu Ile Ile Val Ala Asn Lys His Tyr Pro Leu Ser
      50             55             60

Lys Asp Tyr Asn Pro Gly Glu Asn Pro Thr Ala Lys Ala Glu Leu Val
      65             70             75             80

Lys Leu Ile Lys Ala Met Gln Glu Ala Gly Phe Pro Ile Ser Asp His
      85             90             95

Tyr Ser Gly Phe Arg Ser Tyr Glu Thr Gln Thr Lys Leu Tyr Gln Asp
      100            105            110

Tyr Val Asn Gln Asp Gly Lys Ala Ala Ala Asp Arg Tyr Ser Ala Arg
      115            120            125

Pro Gly Tyr Ser Glu His Gln Thr Gly Leu Ala Phe Asp Val Ile Gly
      130            135            140

Thr Asp Gly Asp Leu Val Thr Glu Glu Lys Ala Ala Gln Trp Leu Leu
      145            150            155            160

Asp His Ala Ala Asp Tyr Gly Phe Val Val Arg Tyr Leu Lys Gly Lys
      165            170            175

Glu Lys Glu Thr Gly Tyr Met Ala Glu Glu Trp His Leu Arg Tyr Val
      180            185            190

Gly Lys Glu Ala Lys Glu Ile Ala Ala Ser Gly Leu Ser Leu Glu Glu
      195            200            205

Tyr Tyr Gly Phe Glu Gly Gly Asp Tyr Val Asp
      210            215

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(2) INFORMATION FOR SEQ ID NO: 29:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 790 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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GAAAGGCTCG	TGGTCAATA	ATCTTACCTG	CGGTTATGAT	GAATAATAA	TCTTGGAAAA	60
TATAAATATA	AAAATACCTG	AAGAAAAAAT	ATCAGTTATT	ATTGGGTCAA	ATGGTTGTGG	120
GAAATCAACA	CTCATTAAAA	CCTTGTCTCG	ACTTATAAG	CCATTAGAGG	GAGAAGTATT	180
GCTTGATAAT	AAATCAATTA	ATTCTTATA	AGAAAAAGAT	TTAGCAAAAC	ACATAGCTAT	240
ATTACCTCAA	TCTCCAATA	TCCCTGAATC	AATAACAGTA	GCTGATCTTG	TAAGCCGTGG	300
TCGTTTCCCC	TACAGAAAGC	CTTTTAAGAG	TCTTGGAAAA	GATGACCTTG	AAATAATAAA	360
CAGATCAATG	GTTAAGGCCA	ATGTTGAAGA	TCTAGCAAAAT	AACCTAGTTG	AAGAACCTTC	420
TGGGGGTCAA	AGGCAAGAG	TATGGATAGC	TCTAGCCCTA	GCCCAAGATA	CAAGTATCCT	480
ACTTTTAGAT	GAGCCAATA	CTTACTTGGA	TATCTCATAT	CAATAGAAC	TATTAGACCT	540
CTTGACTGAT	CTAAACCAA	AATATAAGAC	AACCAATTGC	ATGATTTTGC	ACGATATAAA	600
TCTAACAGCA	AGATACGCTG	ATTACCTATT	TGCAATTAAA	GAAAGTAAAC	TTGTTGCAGA	660
GGGAAAGCCT	GAAGATATAC	TAAATGATAA	ACTAGTTAAA	GATATCTTTA	ATCTTGAAGC	720
AAAAATTATA	CGTGACCCTA	TTTCCAATTC	GCCTCTAATG	ATTCTTATTG	GCAAGCACCA	780
TGTTAACTCT						790

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Lys Gly Leu Trp Ser Asn Asn Leu Thr Cys Gly Tyr Asp Glu Lys Ile
1 5 10 15

Ile Leu Glu Asn Ile Asn Ile Lys Ile Pro Glu Glu Lys Ile Ser Val
20 25 30

Ile Ile Gly Ser Asn Gly Cys Gly Lys Ser Thr Leu Ile Lys Thr Leu
35 40 45

Ser Arg Leu Ile Lys Pro Leu Glu Gly Glu Val Leu Leu Asp Asn Lys
50 55 60

Ser Ile Asn Ser Tyr Lys Glu Lys Asp Leu Ala Lys His Ile Ala Ile
65 70 75 80

Leu Pro Gln Ser Pro Ile Ile Pro Glu Ser Ile Thr Val Ala Asp Leu
85 90 95

Val Ser Arg Gly Arg Phe Pro Tyr Arg Lys Pro Phe Lys Ser Leu Gly
 100 105 110

Lys Asp Asp Leu Glu Ile Ile Asn Arg Ser Met Val Lys Ala Asn Val
 115 120 125

Glu Asp Leu Ala Asn Asn Leu Val Glu Glu Leu Ser Gly Gly Gln Arg
 130 135 140

Gln Arg Val Trp Ile Ala Leu Ala Leu Ala Gln Asp Thr Ser Ile Leu
 145 150 155 160

Leu Leu Asp Glu Pro Thr Thr Tyr Leu Asp Ile Ser Tyr Gln Ile Glu
 165 170 175

Leu Leu Asp Leu Leu Thr Asp Leu Asn Gln Lys Tyr Lys Thr Thr Ile
 180 185 190

Cys Met Ile Leu His Asp Ile Asn Leu Thr Ala Arg Tyr Ala Asp Tyr
 195 200 205

Leu Phe Ala Ile Lys Glu Gly Lys Leu Val Ala Glu Gly Lys Pro Glu
 210 215 220

Asp Ile Leu Asn Asp Lys Leu Val Lys Asp Ile Phe Asn Leu Glu Ala
 225 230 235 240

Lys Ile Ile Arg Asp Pro Ile Ser Asn Ser Pro Leu Met Ile Pro Ile
 245 250 255

Gly Lys His His Val Ser
 260

(2) INFORMATION FOR SEQ ID NO: 31:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 781 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

AAACTCAGAA AAGAAAGCAG ACAATGCAAC AACTATCAAA ATCGCAACTG TTAACCGTAG	60
CGGTTCTGAA GAAAAACGTT GGGACAAAAT CCAAGAATTG GTTAAAAAAG ACGGAATATC	120
CTTGGAATTT ACAGAGTTCA CAGACTACTC ACAACCAATC AAAGCAACTG CTGATGGCGA	180
AGTAGATTTG AACGCTTTCC AACACTATAA CTTCTTGAAC AACTGGAACA AAGAAAACGG	240
AAAAGACCTT GTAGCGATTG CAGATACTTA CATCTCTCCA ATCCGCCTTT ACTCAGGTTT	300
GAATGGAAGT GCCAACAAGT AACTAAAGT AGAAGACATC CCAGCAAACG GAGAAATCGC	360
TGTACCGAAT GACGCTACAA ACGAAAGCCG TGCGCTTTAT TTGCTTCAAT CAGCTGGCTT	420
GATTAAATTG GATGTTTCTG GAACTGCTCT TGCAACAGTT GCCAACATCA AAGAAAATCC	480
AAAGAACTTG AAAATCACTG AATTGGACGC TAGCCAAACA GTCGTTTCAT TGTCATCACT	540

TGACGCTGCC GTTGTAAACA ATACCTTCGT TACAGAAGCA AAATTGGACT ACAAGAAATC 600
 ACTTTTCAAA GAACAAGCTG ATGAAAACCTG AAAACAATGG TACAACATCA TTGTTGCAAA 660
 AAAAGATTGG GAAACATCAC CTAAGGCTGA TGCTATCAAG AAAGTAATCG CAGGTTACCA 720
 CACAGATGAC GTGAAAAAAG TTATCGAAGA ATCATCAGAT GGTTTGGATC AACCAGTTTG 780
 G 781

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Asn Ser Glu Lys Lys Ala Asp Asn Ala Thr Thr Ile Lys Ile Ala Thr
 1 5 10 15
 Val Asn Arg Ser Gly Ser Glu Glu Lys Arg Trp Asp Lys Ile Gln Glu
 20 25 30
 Leu Val Lys Lys Asp Gly Ile Thr Leu Glu Phe Thr Glu Phe Thr Asp
 35 40 45
 Tyr Ser Gln Pro Asn Lys Ala Thr Ala Asp Gly Glu Val Asp Leu Asn
 50 55 60
 Ala Phe Gln His Tyr Asn Phe Leu Asn Asn Trp Asn Lys Glu Asn Gly
 65 70 75 80
 Lys Asp Leu Val Ala Ile Ala Asp Thr Tyr Ile Ser Pro Ile Arg Leu
 85 90 95
 Tyr Ser Gly Leu Asn Gly Ser Ala Asn Lys Tyr Thr Lys Val Glu Asp
 100 105 110
 Ile Pro Ala Asn Gly Glu Ile Ala Val Pro Asn Asp Ala Thr Asn Glu
 115 120 125
 Ser Arg Ala Leu Tyr Leu Leu Gln Ser Ala Gly Leu Ile Lys Leu Asp
 130 135 140
 Val Ser Gly Thr Ala Leu Ala Thr Val Ala Asn Ile Lys Glu Asn Pro
 145 150 155 160
 Lys Asn Leu Lys Ile Thr Glu Leu Asp Ala Ser Gln Thr Ala Arg Ser
 165 170 175
 Leu Ser Ser Val Asp Ala Ala Val Val Asn Asn Thr Phe Val Thr Glu
 180 185 190
 Ala Lys Leu Asp Tyr Lys Lys Ser Leu Phe Lys Glu Gln Ala Asp Glu
 195 200 205

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Asn Ser Lys Gln Trp Tyr Asn Ile Ile Val Ala Lys Lys Asp Trp Glu
 210 215 220

Thr Ser Pro Lys Ala Asp Ala Ile Lys Lys Val Ile Ala Ala Tyr His
 225 230 235 240

Thr Asp Asp Val Lys Lys Val Ile Glu Glu Ser Ser Asp Gly Leu Asp
 245 250 255

Gln Pro Val Trp
 260

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 640 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

TTCGAAAGGG TCAGAAGGTG CAGACCTTAT CAGCATGAAA GGGGATGTCA TTACAGAACA 60

TCAATTTTAT GAGCAAGTGA AAAGCAACCC TTCAGCCCAA CAACTCTTGT TAAATATGAC 120

CATCCAAAAA GTTTTGTAAA AACAATATGG CTCAGAGCTT GATGATAAAG AGGTTGATGA 180

TACTATTGCC GAAGAAAAAA AACAATATGG CGAAAACTAC CAACGTGTCT TGTCACAAGC 240

AGGTATGACT CTTGAAACAC GTAAAGCTCA AATTCGTACA AGTAAATAG TTGAGTTGGC 300

AGTTAAGAAG GTACGAGAAG CTGAATTGAC AGATGAAGCC TATAAGAAAG CCTTTGATGA 360

GTACACTCCA GATGTAACGG CTCAAATCAT CCGTCTTAAT AATGAAGATA AGGCCAAAGA 420

AGTTCTCGAA AAGCCCAAGG CAGAAGGTGC TGATTTTGCT CAATTAGCCA AAGATAATTC 480

AACTGATGAA AAAACAAAAG AAAATGGTGG AGAAATTACC TTTGATTCTG CTTCAACAGA 540

AGTACCTGGA GCAAGTCCAA AAAAGCCGCT TTTGCTTTT AGATGTGGGA TGGTGTCTTCT 600

GGATGTGGAT TACAGCAACT GGGGCACACC AAGCCTACAG 640

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Ser Lys Gly Ser Glu Gly Ala Asp Leu Ile Ser Met Lys Gly Asp Val
 1 5 10 15

Ile Thr Glu His Gln Phe Tyr Glu Gln Val Lys Ser Asn Pro Ser Ala

20

25

30

Gln Gln Val Leu Leu Asn Met Thr Ile Gln Lys Val Phe Glu Lys Gln
 35 40 45

Tyr Gly Ser Glu Leu Asp Asp Lys Glu Val Asp Asp Thr Ile Ala Glu
 50 55 60

Glu Lys Lys Gln Tyr Gly Glu Asn Tyr Gln Arg Val Leu Ser Gln Ala
 65 70 75 80

Gly Met Thr Leu Glu Thr Arg Lys Ala Gln Ile Arg Thr Ser Lys Leu
 85 90 95

Val Glu Leu Ala Val Lys Lys Val Ala Glu Ala Glu Leu Thr Asp Glu
 100 105 110

Ala Tyr Lys Lys Ala Phe Asp Glu Tyr Thr Pro Asp Val Thr Ala Gln
 115 120 125

Ile Ile Arg Leu Asn Asn Glu Asp Lys Ala Lys Glu Val Leu Glu Lys
 130 135 140

Ala Lys Ala Glu Gly Ala Asp Phe Ala Gln Leu Ala Lys Asp Asn Ser
 145 150 155 160

Thr Asp Glu Lys Thr Lys Glu Asn Gly Gly Glu Ile Thr Phe Asp Ser
 165 170 175

Ala Ser Thr Glu Val Pro Gly Ala Ser Pro Lys Lys Pro Leu Phe Ala
 180 185 190

Phe Arg Cys Gly Met Val Phe Leu Asp Val Asp Tyr Ser Asn Trp Gly
 195 200 205

Thr Pro Ser Leu Gln
 210

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 631 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

GGGGATGGCA GCTTTTAAAA ATCCTAACAA TCANTACAAA GCTATTACAA TTGCTCAAAC 60

TCTAGGTGAT GATGCTTCTT CAGAGGAATT GGCTGGTAGA TATGGTTCTG CTGTTCAAGT 120

TACAGAAGTG ACTGCCTCAA ACCTTTCAAC AGTTAAAACT AAAGCTACGG TTGTAGAAAA 180

ACCACTGAAA GATTTTAGAG CGTCTACGTC TGATCACTCT GGTGGGGTGG AATCTAATGG 240

TAAATGGTAT TTCTATGAGT CTGGTGATGT GAAGACAGGT TGGGTGAAAA CAGATGGTAA 300

ATGGTACTAT TTGAATGACT TAGGTGTCAT GCAGACTGGA TTTGTAAAAA TTTCTGGTAG 360

CTGGTATTAC TTGAGCAATT CAGGTGCTAT GTTTACAGGC TGGGGAACAG ATGGTAGCAG 420

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ATGGTTCTAC TTGACGGCT CAGGAGCTAT GAAGACAGGC TGGTACAAGG AAAATGGCAC 480
 TTGGTATTAC CTTGACGAAG CAGGTATCAT GAAGACAGGT TGGTTTAAAG TCGGACCACA 540
 CTGGTACTAT GCCTACGGTT CAGGAGCTTT GGCTGTGAGC ACAACAACAC CAGATGGTTA 600
 CCGTGTAAT GGTAATGGTG AATGGGTAAA C 631

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 210 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Gly Met Ala Ala Phe Lys Asn Pro Asn Asn Gln Tyr Lys Ala Ile Thr
 1 5 10 15
 Ile Ala Gln Thr Leu Gly Asp Asp Ala Ser Ser Glu Glu Leu Ala Gly
 20 25 30
 Arg Tyr Gly Ser Ala Val Gln Cys Thr Glu Val Thr Ala Ser Asn Leu
 35 40 45
 Ser Thr Val Lys Thr Lys Ala Thr Val Val Glu Lys Pro Leu Lys Asp
 50 55 60
 Phe Arg Ala Ser Thr Ser Asp Gln Ser Gly Trp Val Glu Ser Asn Gly
 65 70 75 80
 Lys Trp Tyr Phe Tyr Glu Ser Gly Asp Val Lys Thr Gly Trp Val Lys
 85 90 95
 Thr Asp Gly Lys Trp Tyr Tyr Leu Asn Asp Leu Gly Val Met Gln Thr
 100 105 110
 Gly Phe Val Lys Phe Ser Gly Ser Trp Tyr Tyr Leu Ser Asn Ser Gly
 115 120 125
 Ala Met Phe Thr Gly Trp Gly Thr Asp Gly Ser Arg Trp Phe Tyr Phe
 130 135 140
 Asp Gly Ser Gly Ala Met Lys Thr Gly Trp Tyr Lys Glu Asn Gly Thr
 145 150 155 160
 Trp Tyr Tyr Leu Asp Glu Ala Gly Ile Met Lys Thr Gly Trp Phe Lys
 165 170 175
 Val Gly Pro His Trp Tyr Tyr Ala Tyr Gly Ser Gly Ala Leu Ala Val
 180 185 190
 Ser Thr Thr Thr Pro Asp Gly Tyr Arg Val Asn Gly Asn Gly Glu Trp
 195 200 205

--Val Asn
 210

00765272.012001

(2) INFORMATION FOR SEQ ID NO: 37:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1360 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

AGACGAGCAA AAAATTAAGC AAGCAGAAGC GGAAGTTGAG AGTAAACAAG CTGAGGCTAC 60
 AAGGTTAAAA AAAATCAAGA CAGATCGTGA AGAAGCAGAA GAAGAAGCTA AACGAAGAGC 120
 AGATGCTAAA GAGCAAGGTA AACCAAAGGG GCGGGCAAAA CGAGGAGTTC CTGGAGAGCT 180
 AGCAACACCT GATAAAAAAG AAAATGATGC GAAGTCTTCA GATTCAGCG TAGTGGAAGA 240
 AACTCTTCCA AGCCCATCCC TGAAACCAGA AAAAAAGGTA GCAGAAGCTG AGAAGAAGGT 300
 TGAAGAAGCT AAGAAAAAAG CCGAGGATCA AAAAGAAGAA GATCGCCGTA ACTACCCAAC 360
 CAATACTTAC AAAACGCTTG AACTTGAAAT TGCTGAGTCC GATGTGGAAG TTAATAAAGC 420
 GAGGCTTGAA CTAGTAAAAG AGGAAGCTAA GGAACCTCGA AACGAGGAAA AAGTTAAGCA 480
 AGCAAAAGCG GAAGTTGAGA GTAAAAAAGC TGAGGCTACA AGGTTAGAAA AAATCAAGAC 540
 AGATCGTAAA AAAGCAGAAG AAGAAGCTAA ACGAAAAGCA GCAGAAGAAG ATAAAGTTAA 600
 AGAAAAACCA GCTGAACAAC CACAACCAGC GCCGGCTCCA AAAGCAGAAA AACCAGCTCC 660
 AGCTCCAAAA CCAGAGAATC CAGCTGAACA ACCAAAAGCA GAAAAACCAG CTGATCAACA 720
 AGCTGAAGAA GACTATGCTC GTAGATCAGA AGAAGAATAT AATCGCTTGA CTCACAGCA 780
 ACCGCCAAAA ACTGAAAAAC CAGCACCAAC ATCTACTCCA AAACAGGCTT GGAACAAGA 840
 AAACGGTATG TGGTACTTCT ACAATACTGA TGGTTCAATG GCGACAGGAT GGCTCCAAAA 900
 CAATGGCTCA TGGTACTACC TCAACAGCAA TGGCGCTATG GCGACAGGAT GGCTCCAAAA 960
 CAATGGTTCA TGGTACTATC TAAACGCTAA TGGTTCAATG GCAACAGGAT GGCTCCAAAA 1020
 CAATGGTTCA TGGTACTACC TAAACGCTAA TGGTTCAATG GCGACAGGAT GGCTCCAAAA 1080
 CAATGGCTCA TGGTACTACC TAAACGCTAA TGGTTCAATG GCGACAGGAT GGCTCCAAAA 1140
 CAATGGCTCA TGGTACTACC TAAACGCTAA TGGTGATATG GCGACAGGAT GGGTGAAAGA 1200
 TGGAGATACC TGGTACTATC TTGAAGCATC AGGTGCTATG AAAGCAAGCC AATGGTTCAA 1260
 AGTATCAGAT AAATGGTACT ATGTCAATGG CTCAGGTGCC CTGCGAGTCA ACACAACTGT 1320
 AGATGGCTAT GGAGTCAATG CCAATGGTGA ATGGGTAAAC 1360

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 453 amino acids

00765272.012201

(B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

```

Asp Glu Gln Lys Ile Lys Gln Ala Glu Ala Glu Val Glu Ser Lys Gln
1      5      10      15
Ala Glu Ala Thr Arg Leu Lys Lys Ile Lys Thr Asp Arg Glu Glu Ala
20      25      30
Glu Glu Glu Ala Lys Arg Arg Ala Asp Ala Lys Glu Gln Gly Lys Pro
35      40      45
Lys Gly Arg Ala Lys Arg Gly Val Pro Gly Glu Leu Ala Thr Pro Asp
50      55      60
Lys Lys Glu Asn Asp Ala Lys Ser Ser Asp Ser Ser Val Gly Glu Glu
65      70      75      80
Thr Leu Pro Ser Pro Ser Leu Lys Pro Glu Lys Lys Val Ala Glu Ala
85      90      95
Glu Lys Lys Val Glu Glu Ala Lys Lys Lys Ala Glu Asp Gln Lys Glu
100     105     110
Glu Asp Arg Arg Asn Tyr Pro Thr Asn Thr Tyr Lys Thr Leu Glu Leu
115     120     125
Glu Ile Ala Glu Ser Asp Val Glu Val Lys Lys Ala Glu Leu Glu Leu
130     135     140
Val Lys Glu Glu Ala Lys Glu Pro Arg Asn Glu Glu Lys Val Lys Gln
145     150     155     160
Ala Lys Ala Glu Val Glu Ser Lys Lys Ala Glu Ala Thr Arg Leu Glu
165     170     175
Lys Ile Lys Thr Asp Arg Lys Lys Ala Glu Glu Glu Ala Lys Arg Lys
180     185     190
Ala Ala Glu Glu Asp Lys Val Lys Glu Lys Pro Ala Glu Gln Pro Gln
195     200     205
Pro Ala Pro Ala Pro Lys Ala Glu Lys Pro Ala Pro Ala Pro Lys Pro
210     215     220
Glu Asn Pro Ala Glu Gln Pro Lys Ala Glu Lys Pro Ala Asp Gln Gln
225     230     235     240
Ala Glu Glu Asp Tyr Ala Arg Arg Ser Glu Glu Glu Tyr Asn Arg Leu
245     250     255
Thr Gln Gln Gln Pro Pro Lys Thr Glu Lys Pro Ala Gln Pro Ser Thr
260     265     270
Pro Lys Thr Gly Trp Lys Gln Glu Asn Gly Met Trp Tyr Phe Tyr Asn
275     280     285

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00765527.012201

Thr Asp Gly Ser Met Ala Thr Gly Trp Leu Gln Asn Asn Gly Ser Trp
 290 295 300

Tyr Tyr Leu Asn Ser Asn Gly Ala Met Ala Thr Gly Trp Leu Gln Asn
 305 310 315 320

Asn Gly Ser Trp Tyr Tyr Leu Asn Ala Asn Gly Ser Met Ala Thr Gly
 325 330 335

Trp Leu Gln Asn Asn Gly Ser Trp Tyr Leu Asn Ala Asn Gly Ser
 340 345 350

Met Ala Thr Gly Trp Leu Gln Tyr Asn Gly Ser Trp Tyr Tyr Leu Asn
 355 360 365

Ala Asn Gly Ser Met Ala Thr Gly Trp Leu Gln Tyr Asn Gly Ser Trp
 370 375 380

Tyr Tyr Leu Asn Ala Asn Gly Asp Met Ala Thr Gly Trp Val Lys Asp
 385 390 395 400

Gly Asp Thr Trp Tyr Tyr Leu Glu Ala Ser Gly Ala Met Lys Ala Ser
 405 410 415

Gln Trp Phe Lys Val Ser Asp Lys Trp Tyr Tyr Val Asn Gly Ser Gly
 420 425 430

Ala Leu Ala Val Asn Thr Thr Val Asp Gly Tyr Gly Val Asn Ala Asn
 435 440 445

Gly Glu Trp Val Asn
 450

(2) INFORMATION FOR SEQ ID NO: 39:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 412 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

CTGTGGTGAG GAAGAACTA AAAAGACTCA AGCAGCACAA CAGCCAAAAC AACAAACGAC 60

TGTACAACAA ATTGCTGTTG GAAAAGATGC TCCAGACTTC ACATTGCAAT CCATGGATGG 120

CAAAGAAGTT AAGTTATCTG ATTTTAAGGG TAAAAAGGTT TACTTGAAGT TTTGGGCTTC 180

ATGTTGTGGT CCATGCAAGA AAAGTATGCC AGAGTTGATG GAACTAGCGG CGAAACCAGA 240

TCGTGATTTC GAAATCTTCA CTGTCAATTG ACCAGGAATT CAAGGTGAAA AAATCTGTTGA 300

GCAATTCCCA CAATGGTTCC AGGAACAAGG ATATAAGGAT ATCCAGTTC TTTATGATAC 360

CAAAGCAACC ACTTCCAAGC TTATCAAATT CGAAGCATTC CTACAGAATA TT 412

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 137 amino acids

00765273.0 1220

- (B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

```

Cys Gly Glu Glu Glu Thr Lys Lys Thr Gln Ala Ala Gln Gln Pro Lys
 1           5           10           15

Gln Gln Thr Thr Val Gln Gln Ile Ala Val Gly Lys Asp Ala Pro Asp
 20           25           30

Phe Thr Leu Gln Ser Met Asp Gly Lys Glu Val Lys Leu Ser Asp Phe
 35           40           45

Lys Gly Lys Lys Val Tyr Leu Lys Phe Trp Ala Ser Trp Cys Gly Pro
 50           55           60

Cys Lys Lys Ser Met Pro Glu Leu Met Glu Leu Ala Ala Lys Pro Asp
 65           70           75           80

Arg Asp Phe Glu Ile Leu Thr Val Ile Ala Pro Gly Ile Gln Gly Glu
 85           90           95

Lys Thr Val Glu Gln Phe Pro Gln Trp Phe Gln Glu Gln Gly Tyr Lys
100           105           110

Asp Ile Pro Val Leu Tyr Asp Thr Lys Ala Thr Thr Ser Lys Leu Ile
115           120           125

Lys Phe Glu Ala Phe Leu Gln Asn Ile
130           135

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(2) INFORMATION FOR SEQ ID NO: 41:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1462 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

```

GACCTTTTAAC AATAAAACTA TTGAAGAGTT GCACAATCTC CTGTCTCTA AGGAAATTC 60
TGCAACAGAA TTGACCCAAG CAACACTTGA AATATCAAG TCTCGTGAGG AAGCCCTCAA 120
TTCATTGTGTC ACCATCGCTG AGGAGCAAGC TCTGTGTCAA GCTAAAGCCA TTGATGAAGC 180
tGGAATGAT GCTGACAATG TCCTTTCAGG AATCCACTT GCTGTTAAGG ATAACATCTC 240
TACAGACGGT ATTTCTCACA CTGCTGCCTC AAAAATGCTC TACAACTATG AGCCAACTTT 300
TGATGCGACA gTgTtGcCA ATGCAAAAAC CAAGGCGATG ATtTtCGTtG GAAAGACCAA 360
CATGGACGAA TTTGCTATGG GTGGTTCAGG tGAAACTTCA CACTACGGAG CAACTAAAAA 420
CGCTTGGAAC CACAGCAAGG TTCCTGGTGG GTCATCAAGT GGTTCGTCCG CAGCTGTAGC 480

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CTCAGGACAA GTTCGCTTGT CACTTGGTTC TGATACTGGT GGTTCATCC GCCAACCTGC 540
 TGCCTTCAAC GGAATCGTTG GTCTCAAACC AACCTACGGA ACAGTTTCAC GTTTCGGTCT 600
 CATTTGCCTTT GGTAGCTCAT TAGACCAGAT TGGACCTTTT GCTCCTACTG TTAAGGAAAA 660
 TGCCCTCTTG CTCAACGCTA TTGCCAGCGA AGATGCTAAA GACTCTACTT CTGCTCCTGT 720
 CCGCATCGCC GACTTTACTT CAAAAATCGG CCAAGACATC AAGGGTATGA AAATCGCTTT 780
 GCCTAAGGAA TACCTAGGCG AAGGAATTGA TCCAGAGGTT AAGGAAACAA TCTTAAACGC 840
 GGCCAAACAC TTTGAAAAT TGGGTGCTAT CGTCGAAGAA GTCAGCCTTC CTCACTCTAA 900
 ATACGCTGTT GCCGTTTATT ACATCATCGC TTCATCAGAA GCTTCATCAA ACTTGCAACG 960
 CTTTCGCGGT ATCCGTTACG GCTATCGCGC AGAAGATGCA ACCAACCTTG ATGAAATCTA 1020
 TGTAAACAGC CGAAGCCAAG GTTTTGGTGA AGAGGTAAAA CGTCGTATCA TGCTGGGTAC 1080
 TTTCACTCTT TCATCAGGTT ACTATGATGC CTACTACAAA AAGGCTGGTC AAGTCCGTAC 1140
 CCTCATCATT CAAGATTTCG AAAAAGTCTT CGCGGATTAC GATTTGATTT TGGGTCCAAC 1200
 TGCTCCAAGT GTTGCTTATG ACTTGGATTC TCTCAACCAT GACCCAGITG CCATGTACTT 1260
 AGCCGACCTA TTGACCATAC CTGTAAACTT GGCAGGACTG CCTGGAATTT CGATTCTTGC 1320
 TGGATTCTCT CAAGGTCTAC CTGTCGGACT CCAATTGATT GGTCCCAAGT ACTCTGAGGA 1380
 AACCATTTAC CAAGTCGCTG CTGCTTTTGA AGCAACAACA GACTACCACA AACAACAACC 1440
 CGTGATTTT GGAGGTGACA AC 1462

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Thr Phe Asn Asn Lys Thr Ile Glu Glu Leu His Asn Leu Leu Val Ser
 1 5 10 15
 Lys Glu Ile Ser Ala Thr Glu Leu Thr Gln Ala Thr Leu Glu Asn Ile
 20 25 30
 Lys Ser Arg Glu Glu Ala Leu Asn Ser Phe Val Thr Ile Ala Glu Glu
 35 40 45
 Gln Ala Leu Val Gln Ala Lys Ala Ile Asp Glu Ala Gly Ile Asp Ala
 50 55 60
 Asp Asn Val Leu Ser Gly Ile Pro Leu Ala Val Lys Asp Asn Ile Ser
 65 70 75 80

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Thr Asp Gly Ile Leu Thr Thr Ala Ala Ser Lys Met Leu Tyr Asn Tyr
 85 90 95
 Glu Pro Ile Phe Asp Ala Thr Ala Val Ala Asn Ala Lys Thr Lys Gly
 100 105 110
 Met Ile Val Val Gly Lys Thr Asn Met Asp Glu Phe Ala Met Gly Gly
 115 120 125
 Ser Gly Glu Thr Ser His Tyr Gly Ala Thr Lys Asn Ala Trp Asn His
 130 135 140
 Ser Lys Val Pro Gly Gly Ser Ser Ser Gly Ser Ala Ala Ala Val Ala
 145 150 155 160
 Ser Gly Gln Val Arg Leu Ser Leu Gly Ser Asp Thr Gly Gly Ser Ile
 165 170 175
 Arg Gln Pro Ala Ala Phe Asn Gly Ile Val Gly Leu Lys Pro Thr Tyr
 180 185 190
 Gly Thr Val Ser Arg Phe Gly Leu Ile Ala Phe Gly Ser Ser Leu Asp
 195 200 205
 Gln Ile Gly Pro Phe Ala Pro Thr Val Lys Glu Ala Leu Leu Leu
 210 215 220
 Asn Ala Ile Ala Ser Glu Asp Ala Lys Asp Ser Thr Ser Ala Pro Val
 225 230 235 240
 Arg Ile Ala Asp Phe Thr Ser Lys Ile Gly Gln Asp Ile Lys Gly Met
 245 250 255
 Lys Ile Ala Leu Pro Lys Glu Tyr Leu Gly Glu Gly Ile Asp Pro Glu
 260 265 270
 Val Lys Glu Thr Ile Leu Asn Ala Ala Lys His Phe Glu Lys Leu Gly
 275 280 285
 Ala Ile Val Glu Glu Val Ser Leu Pro His Ser Lys Tyr Gly Val Ala
 290 295 300
 Val Tyr Tyr Ile Ile Ala Ser Ser Glu Ala Ser Ser Asn Leu Gln Arg
 305 310 315 320
 Phe Asp Gly Ile Arg Tyr Gly Tyr Arg Ala Glu Asp Ala Thr Asn Leu
 325 330 335
 Asp Glu Ile Tyr Val Asn Ser Arg Ser Gln Gly Phe Gly Glu Glu Val
 340 345 350
 Lys Arg Arg Ile Met Leu Gly Thr Phe Ser Leu Ser Ser Gly Tyr Tyr
 355 360 365
 Asp Ala Tyr Tyr Lys Lys Ala Gly Gln Val Arg Thr Leu Ile Ile Gln
 370 375 380
 Asp Phe Glu Lys Val Phe Ala Asp Tyr Asp Leu Ile Leu Gly Pro Thr
 385 390 395 400
 Ala Pro Ser Val Ala Tyr Asp Leu Asp Ser Leu Asn His Asp Pro Val
 405 410 415

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Ala Met Tyr Leu Ala Asp Leu Leu Thr Ile Pro Val Asn Leu Ala Gly
 420 425 430

Leu Pro Gly Ile Ser Ile Pro Ala Gly Phe Ser Gln Gly Leu Pro Val
 435 440 445

Gly Leu Gln Leu Ile Gly Pro Lys Tyr Ser Glu Glu Thr Ile Tyr Gln
 450 455 460

Ala Ala Ala Ala Phe Glu Ala Thr Thr Asp Tyr His Lys Gln Gln Pro
 465 470 475 480

Val Ile Phe Gly Gly Asp Asn
 485

(2) INFORMATION FOR SEQ ID NO: 43:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 433 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

CTTTACAGGT AAACAACCTAC AAGTCGGCGA CAAGGCGCTT GATTTTCTC TTACTACAAC 60

AGATCTTTCT AAAAAATCTC TGGCTGATTT TGATGGCAAG AAAAAAGTCT TGAGTGTCTG 120

TCCTTCTATC GATACAGGCA TCTGCTCAAC TCAAACACGT CGTTTTAATG AAGAATTGGC 180

TGGACTGGAC AACACGGTCG TATTGACTGT TTCAATGGAC CTACCTTTTG CTCAAAAACG 240

TTGGTGCGET GCTGAAGGCC TTGACAATGC CATTATGCTT TCAGACTACT TTGACCATT 300

TTTCGGGCGC GATTATGCCC TCTTGATCAA CGAATGGCAC CTATTAGCAC GCGCAGTCTT 360

TGTCCTCGAT ACTGACAATA CGATTGCTA CGTTGAATAC GTGGATAATA TCAATTCTGA 420

GCCAAACTTC GAA 433

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 144 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Phe Thr Gly Lys Gln Leu Gln Val Gly Asp Lys Ala Leu Asp Phe Ser
 1 5 10 15

Leu Thr Thr Thr Thr Asp Leu Ser Lys Lys Ser-Leu Ala Asp Phe Asp Gly
 20 25 30

Lys Lys Lys Val Leu Ser Val Val Pro Ser Ile Asp Thr Gly Ile Cys

35	40	45
Ser Thr Gln Thr Arg Arg Phe Asn Glu Glu Leu Ala Gly Leu Asp Asn		
50	55	60
Thr Val Val Leu Thr Val Ser Met Asp Leu Pro Phe Ala Gln Lys Arg		
65	70	80
Trp Cys Gly Ala Glu Gly Leu Asp Asn Ala Ile Met Leu Ser Asp Tyr		
85	90	95
Phe Asp His Ser Phe Gly Arg Asp Tyr Ala Leu Leu Ile Asn Glu Trp		
100	105	110
His Leu Leu Ala Arg Ala Val Phe Val Leu Asp Thr Asp Asn Thr Ile		
115	120	125
Arg Tyr Val Glu Tyr Val Asp Asn Ile Asn Ser Glu Pro Asn Phe Glu		
130	135	140

(2) INFORMATION FOR SEQ ID NO: 45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 724 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

CCAGGCTGAT ACAAGTATCG CAGACATTCA AAAAAGAGGC GAAGTGGTTG TCGGTGTCAA	60
ACAAGACGTT CCCAATTITT GTTACAANGA TCCCAAGACC GGTACTTATT CTGGTATCGA	120
AaCCGACTTG GCCAAGATGG TAGCTGATGA ACTCAAGGTC AAGATTTCGCT ATGTGCCGGT	180
TACAGCACAA ACCCGCGGCC CCCTTCTAGA CAATGAACAG GTCGATATGG ATATCGCGAC	240
CTTTACCATC ACGGACGAAC GCAAAAAACT CTACAACTTT ACCAGTCCCT ACTACACAGA	300
CGCTTCTGGA TTTTGTGTCA ATAAATCTGC CAAAATCAAA AAGATTGAGG ACCTAAACGG	360
CAAAACCATC GGAGTCGCCC AAGGTTCTAT CACCCAAGCG CTGATTACTG AACTGGGTAA	420
AAAGAAAGGT CTGAAGTTTA AATTGCTCGA ACTTGTTTCC TACCAGAAT TGATTACTTC	480
CCTGCACGCT CATCGTATCG ATACCTTTTC CGTTGACCGC TCTATTCTAT CTGGTACAC	540
TAGTAAACGG ACAGCACTAC TAGATGATAG TTTCAAGCCA TGTGACTACG GTATTGTTAC	600
CAAGAAATCA AATACAGAGC TCAACGACTA TCTTGATAAC TTGTTACTA AATGGAGCAA	660
GGATGGTAGT TTGCAGAAAC TTTATGACCG TTACAAGCTC AAACCATCTA GCCATATGCG	720
AGAT	724

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 amino acids
- (B) TYPE: amino acid

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(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Gln Ala Asp Thr Ser Ile Ala Asp Ile Gln Lys Arg Gly Glu Leu Val
1 5 10 15
Val Gly Val Lys Gln Asp Val Pro Asn Phe Gly Tyr Xaa Asp Pro Lys
20 25 30
Thr Gly Thr Tyr Ser Gly Ile Glu Thr Asp Leu Ala Lys Met Val Ala
35 40 45
Asp Glu Leu Lys Val Lys Ile Arg Tyr Val Pro Val Thr Ala Gln Thr
50 55 60
Arg Gly Pro Leu Leu Asp Asn Glu Gln Val Asp Met Asp Ile Ala Thr
65 70 75 80
Phe Thr Ile Thr Asp Glu Arg Lys Lys Leu Tyr Asn Phe Thr Ser Pro
85 90 95
Tyr Tyr Thr Asp Ala Ser Gly Phe Leu Val Asn Lys Ser Ala Lys Ile
100 105 110
Lys Lys Ile Glu Asp Leu Asn Gly Lys Thr Ile Gly Val Ala Gln Gly
115 120 125
Ser Ile Thr Gln Arg Leu Ile Thr Glu Leu Gly Lys Lys Lys Gly Leu
130 135 140
Lys Phe Lys Phe Val Glu Leu Gly Ser Tyr Pro Glu Leu Ile Thr Ser
145 150 155 160
Leu His Ala His Arg Ile Asp Thr Phe Ser Val Asp Arg Ser Ile Leu
165 170 175
Ser Gly Tyr Thr Ser Lys Arg Thr Ala Leu Leu Asp Asp Ser Phe Lys
180 185 190
Pro Ser Asp Tyr Gly Ile Val Thr Lys Lys Ser Asn Thr Glu Leu Asn
195 200 205
Asp Tyr Leu Asp Asn Leu Val Thr Lys Trp Ser Lys Asp Gly Ser Leu
210 215 220
Gln Lys Leu Tyr Asp Arg Tyr Lys Leu Lys Pro Ser Ser His Thr Ala
225 230 235 240
Asp

(2) INFORMATION FOR SEQ ID NO: 47:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1279 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

00765272.032204

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

GTCTGTATCA TTTGAAACA AAGAAACAAA CCGTGGTGTC TTgACTTTCA CTATCTCTCA 60
 AGACCAAATC AAACCAGAAT TGGACCGTGT CTTCAAGTCA GTGAAGAAAT CTCCTTAATGT 120
 TCCAGGTTTC CGTAAAGGTC ACCTTCCACG CCTATCTTC GACCAGAAAT TTGGTGAAGA 180
 AGCTCTTTAT CAAGATGCAA TGAACGCACT TTGCCCCAAC GCTTATGAAG CAGCTGTAAA 240
 AGAAGCTGGT CTTGAAGTGG TTGCCCAACC AAAAATTGAC GTAACCTCAA TGGAAAAAAGG 300
 TCAAGACTGG GTTATCACTG CTGAAGTCGT TACAAAACCT GAAGTAAAT TGGGTGACTA 360
 CAAAAACCTT GAAGTATCAG TTGATGTAGA AAAAGAAGTA ACTGACGCTG ATGTCGAAGA 420
 GCGTATCGAA CGCGAACGCA ACAACCTGGC TGAATTGGTT ATCAAGGAAG CTGCTGCTGA 480
 AAACGCGCAG ACTGTTGTGA TCGACTTCGT TGGTTCTATC GACGGTGTG AATTGTACGG 540
 TGGAAAAAGT GAAAACCTCT CACTTGGACT TGTTTCAGGT CAATTCATCC CTGGTTTCGA 600
 AGACCAATGT GTAGTCACT CAGCTGGCGA AACCGTTGAT GTTATCGTAA CATTCACAGA 660
 AGACTACCAA GCAGAAGACC TTGCAGGTAA AGAAGCTAAA TTCGTGACAA CTATCCACGA 720
 AGTAAAGACT AAAGAAGTTC CGGCTCTTGA CGATGAACCT GCAAAAGACA TTGATGAAGA 780
 AGTTGAACA CTTGCTGACT TGAAGAGAAA ATACAGCAAA GAATTGGCTG CTGCTAAAGA 840
 AGAAGCTTAC AAAGATGCAG TTGAAGGTGC AGCAATTGAT ACAGCTGTAG AAAATGCTGA 900
 AATCGTAGAA CTTCAGAAAG AAATGATCCA TGAAGAAGTT CACCGTTCAG TAAATGAATT 960
 CCTTGGGAAT TTGCAACGTC AAGGGATCAA CCCTGACATG TACTTCCAAA TCACCTGGAAC 1020
 TACTCAAGAA GACCTTCACA ACCAATACCA AGCAGAAGCT GAGTCACGTA CTAAGACTAA 1080
 CCTTGTATAT GAAGCAGTTG CCAAGCTGA AGGATTGAT GCTTCAGAAG AAGAAATCCA 1140
 AAAAGAAGTT GAGCAATTGG CAGCAGACTA CAACATGGAA GTTGACAAAG TTCAAAACTT 1200
 GCTTTCAGCT GACATGTTGA AACATGATAT CACTATCAAA AAAGCTGTTG AATTGATCAC 1260
 AAGCACAGCA ACAGTAAAA 1279

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Ser Val Ser Phe Glu Asn Lys Glu Thr Asn Arg Gly Val Leu Thr Phe

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1					5					10						15
Thr	Ile	Ser	Gln	Asp	Gln	Ile	Lys	Pro	Glu	Leu	Asp	Arg	Val	Phe	Lys	
			20					25					30			
Ser	Val	Lys	Lys	Ser	Leu	Asn	Val	Pro	Gly	Phe	Arg	Lys	Gly	His	Leu	
			35				40					45				
Pro	Arg	Pro	Ile	Phe	Asp	Gln	Lys	Phe	Gly	Glu	Glu	Ala	Leu	Tyr	Gln	
						55					60					
Asp	Ala	Met	Asn	Ala	Leu	Leu	Pro	Asn	Ala	Tyr	Glu	Ala	Ala	Val	Lys	
65					70					75					80	
Glu	Ala	Gly	Leu	Glu	Val	Val	Ala	Gln	Pro	Lys	Ile	Asp	Val	Thr	Ser	
				85					90					95		
Met	Glu	Lys	Gly	Gln	Asp	Trp	Val	Ile	Thr	Ala	Glu	Val	Val	Thr	Lys	
			100					105					110			
Pro	Glu	Val	Lys	Leu	Gly	Asp	Tyr	Lys	Asn	Leu	Glu	Val	Ser	Val	Asp	
			115				120					125				
Val	Glu	Lys	Glu	Val	Thr	Asp	Ala	Asp	Val	Glu	Glu	Arg	Ile	Glu	Arg	
			130			135					140					
Glu	Arg	Asn	Asn	Leu	Ala	Glu	Leu	Val	Ile	Lys	Glu	Ala	Ala	Ala	Glu	
145					150					155					160	
Asn	Gly	Asp	Thr	Val	Val	Ile	Asp	Phe	Val	Gly	Ser	Ile	Asp	Gly	Val	
				165					170					175		
Glu	Phe	Asp	Gly	Gly	Lys	Gly	Glu	Asn	Phe	Ser	Leu	Gly	Leu	Gly	Ser	
			180					185					190			
Gly	Gln	Phe	Ile	Pro	Gly	Phe	Glu	Asp	Gln	Leu	Val	Gly	His	Ser	Ala	
			195				200					205				
Gly	Glu	Thr	Val	Asp	Val	Ile	Val	Thr	Phe	Pro	Glu	Asp	Tyr	Gln	Ala	
			210			215					220					
Glu	Asp	Leu	Ala	Gly	Lys	Glu	Ala	Lys	Phe	Val	Thr	Thr	Ile	His	Glu	
225					230					235					240	
Val	Lys	Ala	Lys	Glu	Val	Pro	Ala	Leu	Asp	Asp	Glu	Leu	Ala	Lys	Asp	
				245				250						255		
Ile	Asp	Glu	Glu	Val	Glu	Thr	Leu	Ala	Asp	Leu	Lys	Glu	Lys	Tyr	Ser	
			260					265					270			
Lys	Glu	Leu	Ala	Ala	Ala	Lys	Glu	Glu	Ala	Tyr	Lys	Asp	Ala	Val	Glu	
			275				280					285				
Gly	Ala	Ala	Ile	Asp	Thr	Ala	Val	Glu	Asn	Ala	Glu	Ile	Val	Glu	Leu	
			290			295					300					
Pro	Glu	Glu	Met	Ile	His	Glu	Glu	Val	His	Arg	Ser	Val	Asn	Glu	Phe	
305					310					315					320	
Leu	Gly	Asn	Leu	Gln	Arg	Gln	Gly	Ile	Asn	Pro	Asp	Met	Tyr	Phe	Gln	
			325					330						335		
Ile	Thr	Gly	Thr	Thr	Gln	Glu	Asp	Leu	His	Asn	Gln	Tyr	Gln	Ala	Glu	

159

340

345

350

Ala Glu Ser Arg Thr Lys Thr Asn Leu Val Ile Glu Ala Val Ala Lys
355 360 365

Ala Glu Gly Phe Asp Ala Ser Glu Glu Glu Ile Gln Lys Glu Val Glu
370 375 380

Gln Leu Ala Ala Asp Tyr Asn Met Glu Val Ala Gln Val Gln Asn Leu
385 390 395 400

Leu Ser Ala Asp Met Leu Lys His Asp Ile Thr Ile Lys Lys Ala Val
405 410 415

Glu Leu Ile Thr Ser Thr Ala Thr Val Lys
420 425

(2) INFORMATION FOR SEQ ID NO: 49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 490 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

TGGTCAAAG GAAAGTCAGA CAGGAAAGGG GATGAAAATT GTGACCAGTT TTTATCCTAT	60
CTACGCTATG GTTAAAGGAAG TATCTGGTGA CTGGAATGAT GTTCGGATGA TTCAGTCAAG	120
TAGTGGTATT CACTCCTTTG AACCTTCGGC AAATGATATC GCAGCCATCT ATGATGCAGA	180
TGICTTTGTT TACCATTCTC ATACACTCGA ATCTTGGGCA GGAAGTCTGG ATCCAAATCT	240
AAAAAATCC AAAGTGAAGG TCTTAGAGGC TTCTGAGGGA ATGACCTTGG AACGTGTCCC	300
TGGACTAGAG GATGTGGAAG CAGGGGATGG AGTTGATGAA AAAACGCTCT ATGACCCCTCA	360
CACATGGCTA GATCTGAAA AAGCTGGAGA AGAAGCCCAA ATTATCGCTG ATAAACTTTC	420
AGAGGTGGAT AGTGAGCATA AAGAGACTTA TCAAAAAAAT GCGCAACCTT TATCAAAAAA	480
GCTCAGGAAT	490

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Gly Gln Lys Glu Ser Gln Thr Gly Lys Gly Met Lys Ile Val Thr Ser
1 5 10 15

Phe Tyr Pro Ile Tyr Ala Met Val Lys Glu Val Ser Gly Asp Leu Asn
 20 25 30
 Asp Val Arg Met Ile Gln Ser Ser Ser Gly Ile His Ser Phe Glu Pro
 35 40 45
 Ser Ala Asn Asp Ile Ala Ala Ile Tyr Asp Ala Asp Val Phe Val Tyr
 50 55 60
 His Ser His Thr Leu Glu Ser Trp Ala Gly Ser Leu Asp Pro Asn Leu
 65 70 75 80
 Lys Lys Ser Lys Val Lys Val Leu Glu Ala Ser Glu Gly Met Thr Leu
 85 90 95
 Glu Arg Val Pro Gly Leu Glu Asp Val Glu Ala Gly Asp Gly Val Asp
 100 105 110
 Glu Lys Thr Leu Tyr Asp Pro His Thr Trp Leu Asp Pro Glu Lys Ala
 115 120 125
 Gly Glu Glu Ala Gln Ile Ile Ala Asp Lys Leu Ser Glu Val Asp Ser
 130 135 140
 Glu His Lys Glu Thr Tyr Gln Lys Asn Ala Gln Pro Leu Ser Lys Lys
 145 150 155 160
 Leu Arg Asn

(2) INFORMATION FOR SEQ ID NO: 51:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1006 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

GAAGGATAGA TATATTTTAG CATITGAGAC ATCCTGTGAT GAGACCACTG TCGCCGCTCTT	60
GAAAAACGAC GATGAGCTCT TGTCCAATGT CATTGCTAGT CAAATTGAGA GTCACAAACG	120
TTTTGGTGGC GTAGTGCCCG AAGTAGCCAG TCGTCACCAT GTCGAGGTCA TTACAGCCTG	180
TATCGAGGAG GCATTGGCAG AAGCAGGGAT TACCGAAGAG GACGTGACAG CTGTTGCGGT	240
TACCTACGGA CCAGGCTTGG TCGGAGCCTT GCTAGTTGGT TTGTCACTGG CCAAGGCCTT	300
TGCTTGGGCT CACGACTTC CACTGATTCC TGTTAATCAC ATGGCTGGGC ACCTCATGSC	360
AGCTCAGAGT GTGGAGCCTT TGGAGTTTCC CTGCTAGACC CTCTTGGTCA GCGGCGGACA	420
CACAGAGTTG GTTTATGTTT CGGAGGCAGG AGATTATAAG ATTGTTGGGG AAACCCGTGA	480
TGATGCGGTT GGTGAGGCTT ATGATAAGGT CGGCCGTGTC ATGGGCTTGA CCTATCTGC	540
AGTCTGTGAG ATTGACGAGC TGGCTCATCA GGGGCAGGAT ATTTATGATT TCCCCGCTGC	600
CATGATTAAG GAAGATAATC TGGAGTTCTC CTTCTCAGGT TTGAAATCTG CCTTTATCAA	660

376572-01201
 10210-272892

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TCTTCATCAC AATGCCGAGC AAAAGGGAGA AAGCCTGTCT ACAGAAGATT TGTGTGCTTC      720
CTTCCAAGCA GCAGTTATGG ACATTCTCAT GGCAAAAACC AAGAAGGCTT TGGAGAAATA      780
TCCTGTATAA ATCCTAGTTG TGGCAGGTGG TGTGGCAGCC AATAAAGGTC TCAGAGAACG      840
CCTAGCAGCC GAAATCACAG ATGTCAAGGT TATCATCCCC CCTCTGCGAC TCTGCGGAGA      900
CAATGCAGGT ATGATTGCTT ATGCCAGCGT CAGCNAGTGG AACAAAGAAA ACTTCGCAGG      960
CTGGGACCTC AATGCCAAAC CAAGTCTTGC CTTTGATACC ATGGAA                      1006

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(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

```

Lys Asp Arg Tyr Ile Leu Ala Phe Glu Thr Ser Cys Asp Glu Thr Ser
 1              5              10              15
Val Ala Val Leu Lys Asn Asp Asp Glu Leu Leu Ser Asn Val Ile Ala
      20              25              30
Ser Gln Ile Glu Ser His Lys Arg Phe Gly Gly Val Val Pro Glu Val
      35              40              45
Ala Ser Arg His His Val Glu Val Ile Thr Ala Cys Ile Glu Glu Ala
      50              55              60
Leu Ala Glu Ala Gly Ile Thr Glu Glu Asp Val Thr Ala Val Ala Val
      65              70              75              80
Thr Tyr Gly Pro Gly Leu Val Gly Ala Leu Leu Val Gly Leu Ser Ala
      85              90              95
Ala Lys Ala Phe Ala Trp Ala His Gly Leu Pro Leu Ile Pro Val Asn
      100             105             110
His Met Ala Gly His Leu Met Ala Ala Gln Ser Val Glu Pro Leu Glu
      115             120             125
Phe Pro Leu Leu Ala Leu Leu Val Ser Gly Gly His Thr Glu Leu Val
      130             135             140
Tyr Val Ser Glu Ala Gly Asp Tyr Lys Ile Val Gly Glu Thr Arg Asp
      145             150             155             160
Asp Ala Val Gly Glu Ala Tyr Asp Lys Val Gly Arg Val Met Gly Leu
      165             170             175
Thr Tyr Pro Ala Gly Arg Glu Ile Asp Glu Leu Ala His Gln Gly Gln
      180             185             190
Asp Ile Tyr Asp Phe Pro Arg Ala Met Ile Lys Glu Asp Asn Leu Glu

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076577-01204

195	200	205
Phe Ser Phe Ser Gly Leu Lys Ser Ala Phe Ile Asn Leu His His Asn		
210	215	220
Ala Glu Gln Lys Gly Glu Ser Leu Ser Thr Glu Asp Leu Cys Ala Ser		
225	230	235 240
Phe Gln Ala Ala Val Met Asp Ile Leu Met Ala Lys Thr Lys Lys Ala		
	245	250 255
Leu Glu Lys Tyr Pro Val Lys Ile Leu Val Val Ala Gly Gly Val Ala		
	260	265 270
Ala Asn Lys Gly Leu Arg Glu Arg Leu Ala Ala Glu Ile Thr Asp Val		
	275	280 285
Lys Val Ile Ile Pro Pro Leu Arg Leu Cys Gly Asp Asn Ala Gly Met		
	290	295 300
Ile Ala Tyr Ala Ser Val Ser Xaa Trp Asn Lys Glu Asn Phe Ala Gly		
	305	310 315 320
Trp Asp Leu Asn Ala Lys Pro Ser Leu Ala Phe Asp Thr Met Glu		
	325	330 335

(2) INFORMATION FOR SEQ ID NO: 53:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1000 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

GGTAGITAAA GTTGGTATTA ACGGTTTCGG ACGTATCGGT CGTCTTGCTT TCCGTCGTAT	60
CCAAAACGTA GAAGTGTTG AAGTTACAG CATCAACGAC CTTACAGATC CAGTTATGCT	120
TGCACACTTG TTGAAATACG ACACAACCTCA AGGTCGTTTC GACGGTACTG TTGAAGTTAA	180
AGAAGTGTTGA TTTGAAGTTA ACGGTAAATT CATCAAAGTT TCTGCTGAAC GTGATCCAGA	240
ACAAATCGAC TGGGCTACTG ACGGTGTAGA AATCGTTCTT GAAGTACTG GTTCTTTTGC	300
TAAGAAAGAA GCAGCTGAAA AACACCTTAA AGGTGGAGCT AAAAAAGTTG TTATCACTGC	360
TCCTGTGTGA AACGACGTTA AAACAGTTGT ATTCAACACT AACCACGACG TCTTTGACGG	420
TACTGAAACA GTTATCTCAG GTGCTTCATG TACTACAAC TGCTTGGCTC CAATGGCTAA	480
AGCTCTTCAA GACAACCTTG GTGTTGTTGA AGGATTGATG ACTACTATCC ACGCTTACAC	540
TGGTGACCAA ATGATCCTTG ACGGACCACA CCGTGGTGST GACCTTCGCC GTGCTCGCGC	600
TGGTGCTGCA AACATCGTTC CTAACCTCAAC TGGTGCTGCA AAAGCTATCG GTCTTTGTAAT	660
CCCAGAATTG AATGGTAAAC TTGACGGATC TGCACAACGC GTTCCAACCT CAACCTGGATC	720
AGTTACTGAA TTGGTAGCAG TTCTTGAAAA GAACGTTACT GTTGATGAAG TGAACGCAGC	780

09765272-012201

TATGAAAGCA GCTTCAAACG AATCATACGG TTACACAGAA GATCCAATCG TATCTTCAGA 840
 TATCGTAGGT ATGTCTTACG GTTCATTGTT TGACGCAACT CAACTAAAG TTCTTGACGT 900
 TGACGGTAAA CAATTGTTTA AAGTTGTATC ATGGTACGAC AACGAAATGT CATACACTGC 960
 ACAACTTGTT CGTACTCTTG GAATACTTCG CAAAAATGCG 1000

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Val Val Lys Val Gly Ile Asn Gly Phe Gly Arg Ile Gly Arg Leu Ala
 1 5 10 15
 Phe Arg Arg Ile Gln Asn Val Glu Gly Val Glu Val Thr Arg Ile Asn
 20 25 30
 Asp Leu Thr Asp Pro Val Met Leu Ala His Leu Leu Lys Tyr Asp Thr
 35 40 45
 Thr Gln Gly Arg Phe Asp Gly Thr Val Glu Val Lys Glu Gly Gly Phe
 50 55 60
 Glu Val Asn Gly Lys Phe Ile Lys Val Ser Ala Glu Arg Asp Pro Glu
 65 70 75 80
 Gln Ile Asp Trp Ala Thr Asp Gly Val Glu Ile Val Leu Glu Ala Thr
 85 90 95
 Gly Phe Phe Ala Lys Lys Glu Ala Ala Glu Lys His Leu Lys Gly Gly
 100 105 110
 Ala Lys Lys Val Val Ile Thr Ala Pro Gly Gly Asn Asp Val Lys Thr
 115 120 125
 Val Val Phe Asn Thr Asn His Asp Val Leu Asp Gly Thr Glu Thr Val
 130 135 140
 Ile Ser Gly Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro Met Ala Lys
 145 150 155 160
 Ala Leu Gln Asp Asn Phe Gly Val Val Glu Gly Leu Met Thr Thr Ile
 165 170 175
 His Ala Tyr Thr Gly Asp Gln Met Ile Leu Asp Gly Pro His Arg Gly
 180 185 190
 Gly Asp Leu Arg Arg Ala Arg Ala Gly Ala Ala Asn Ile Val Pro Asn
 195 200 205
 Ser Thr Gly Ala Ala Lys Ala Ile Gly Leu Val Ile Pro Glu Leu Asn
 210 215 220

09755272-012201

Gly Lys Leu Asp Gly Ser Ala Gln Arg Val Pro Thr Pro Thr Gly Ser
 225 230 235 240
 Val Thr Glu Leu Val Ala Val Leu Glu Lys Asn Val Thr Val Asp Glu
 245 250 255
 Val Asn Ala Ala Met Lys Ala Ala Ser Asn Glu Ser Tyr Gly Tyr Thr
 260 265 270
 Glu Asp Pro Ile Val Ser Ser Asp Ile Val Gly Met Ser Tyr Gly Ser
 275 280 285
 Leu Phe Asp Ala Thr Gln Thr Lys Val Leu Asp Val Asp Gly Lys Gln
 290 295 300
 Leu Val Lys Val Val Ser Trp Tyr Asp Asn Glu Met Ser Tyr Thr Ala
 305 310 315 320
 Gln Leu Val Arg Thr Leu Gly Ile Leu Arg Lys Asn Cys
 325 330

(2) INFORMATION FOR SEQ ID NO: 55:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2389 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

TTCTTACGAC	TTGGGACTGT	ATCAAGCTAG	AACGGTTAAG	GAAAATAATC	GTGTTTCCTA	60
TATAGATGGA	AAACAAGCGA	CGCAAAAAAC	GGAGAATTGG	ACTCCTGATG	AGGTTAGCAA	120
GCGTGAAGGA	ATCAATGCTG	AGCAAAATCGT	CATCAAGATA	ACAGACCAAG	GCTATGTCAC	180
TTACATGGC	GACCACTATC	ATTATTACAA	TGGTAAGGTT	CCTTATGACG	CTATCATCAG	240
TGAAGAATTA	CTCATGAAAG	ATCCAAACTA	TAAGCTAAAA	GATGAGGATA	TGTGTAATGA	300
GGTCAAGGGT	GGATATGTTA	TCAAGGTAGA	TGGAAAATAC	TATGTTTACC	TTAAGGATGC	360
TGCCCACGCG	GATAACGTCC	GTACAAAAGA	GGAAATCAAT	CGACAAAAAC	AAGAGCATAG	420
TCAACATCGT	GAAGTGGGAA	CTCCAAGAAA	CGATGGTGCT	GTGCGCTTGG	CACGTTCCGA	480
AGGACGCTAT	ACTACAGATG	ATGGTTATAT	CTTTAATGCT	TCTGATATCA	TAGAGGATAC	540
TGGTGATGCT	TATATCGTTC	CTCATGGAGA	TCATTACCAT	TACATTCCCTA	AGAATGAGTT	600
ATCAGCTAGC	GAGTTGGCTG	CTGCAGAAGC	CTTCCTATCT	GGTCGAGGAA	ATCTGTCAAA	660
TTCAAGAACC	TATCGCCGAC	AAAATAGCGA	TAACACTTCA	AGAACAAACT	GGGTACCTTC	720
TGTAAGCAAT	CCAGGAACCTA	CAAACTACTA	CACAAGCAAC	AACAGCAACA	CTAAGAGTCA	780
AGCAAGTCAA	AGTAATGACA	TGATAGTCT	CTTGAACACG	CTCTACAAAC	TGCGTTTGAG	840
TCAACGACAT	GTAGAATCTG	ATGGCCTTGT	CTTTGATCCA	GCACAAATCA	CAAGTCGAAC	900
AGCTAGAGGT	GTTGCAGTGC	CACACGGAGA	TCATTACCAC	TTATCCCTT	ACTCTCAAAT	960

10210-225260

GTCTGAATTG GAAGAACGAA TCGCTCGTAT TAITCCCCCTT CGTTATCGTT CAAACCATTG 1020
 GGTACCAGAT TCAAGGCCAG AACACCAAG TCCACAACCG ACTCCGGAAC CTAGTCCAGG 1080
 CCCGCAACCT GCACCAATC TTAATAAGTA CTCAAAATCT TCTTTGGTTA GTCAGTGGT 1140
 ACGAAAAAGTT GGGGAAGGAT ATGTATTCGA AGAAAAGGGC ATCTCTCGTT ATGCTCTTGC 1200
 GAAAGATTTA CCATCTGAAA CTGTTAAAAA TCTTGAAAGC AAGTTATCAA AACAGAGAG 1260
 TGTTCACAC ACTTTAACTG CTAATAAAGA AATGTTGCT CCTCGTGACC AAGAAATTTTA 1320
 TGATAAAGCA TATAATCTGT TAACCTGAGG TCATAAAGCC TTGTTTGNAA ATAAGGGTGC 1380
 TAATTCGTAT TTCCAAGCCT TAGACAAATT ATTAGAAGCG TTGAATGATG AATCGACTAA 1440
 TAAAGAAAAA TTGGTAGATG ATTTATIGGC ATTCTAGCA CCAATTACCC ATCCAGAGCG 1500
 ACTTGGCAAA CCAAAATCTC AAATTGAGTA TACTGAAGAC GAAGTTCGTA TTGCTCAATT 1560
 AGCTGATAAG TATACACGT CAGATGGTTA CATTTTGTAT GAACATGATA TAATCAGTGA 1620
 TGAAGGAGAT GCATATGTAA CGCCTCATAT GGGCCATAGT CACTGGATTG GAAAGATAG 1680
 CCTTTCTGAT AAGGAAAAAG TTGCAGCTCA AGCCTATACT AAAGAAAAAG GTATCTTACC 1740
 TCCATCTCCA GACGCAGATG TTAAGCAAA TCCAACTGGA GATAGTGCAG CAGCTATTTA 1800
 CAATCGTGTG AAAGGGGAAA AACGAATTC ACTCGTTTGA CTTCATATA TGGTTGAGCA 1860
 TACAGTTGAG GTTAAAAACG GTAATTTGAT TATCTCTCAT AAGGATCATT ACCATAATAT 1920
 TAAATTTGCT TGGTTTGATG ATCACACATA CAAAGCTCCA AATGGCTATA CCTTGAAGA 1980
 TTTGTTTGGC ACGATTAAGT ACTACGTAGA ACACCCTGAC GAACGTCCAC ATTCTAATGA 2040
 TGGATGGGGC AATGCCAGTG AGCATGTGTT AGGCAAGAAA GACCACAGTG AAGATCCAAA 2100
 TAAGAATCTC AAAGCGGATG AAGAGCCAGT AGAGGAAACA CTGTGTGAGC CAGAAGTCCC 2160
 TCAAGTAGAG ACTGAAAAAG TAGAAGCCCA ACTCAAAGAA GCAGAAGTTT TGCTTGCAGAA 2220
 AGTAACGGAT TCTAGTCTGA AAGCCAATGC AACAGAAACT CTAGCTGGTT TACGAAATAA 2280
 TTTGACTCTT CAAATTATGG ATAACAATAG TATCATGGCA GAAGCAGAAA AATTACTTGC 2340
 GTTGTTAAAA GGAAGTAATC CTTTATCTGT AAGTAAGGAA AAAATAAAC 2389

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 796 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Ser Tyr Glu Leu Gly Leu Tyr Gln Ala Arg Thr Val Lys Glu Asn Asn

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1 5 10 15
 Arg Val Ser Tyr Ile Asp Gly Lys Gln Ala Thr Gln Lys Thr Glu Asn
 20 25 30
 Leu Thr Pro Asp Glu Val Ser Lys Arg Glu Gly Ile Asn Ala Glu Gln
 35 40 45
 Ile Val Ile Lys Ile Thr Asp Gln Gly Tyr Val Thr Ser His Gly Asp
 50 55 60
 His Tyr His Tyr Tyr Asn Gly Lys Val Pro Tyr Asp Ala Ile Ile Ser
 65 70 75 80
 Glu Glu Leu Leu Met Lys Asp Pro Asn Tyr Lys Leu Lys Asp Glu Asp
 85 90 95
 Ile Val Asn Glu Val Lys Gly Gly Tyr Val Ile Lys Val Asp Gly Lys
 100 105 110
 Tyr Tyr Val Tyr Leu Lys Asp Ala Ala His Ala Asp Asn Val Arg Thr
 115 120 125
 Lys Glu Glu Ile Asn Arg Gln Lys Gln Glu His Ser Gln His Arg Glu
 130 135 140
 Gly Gly Thr Pro Arg Asn Asp Gly Ala Val Ala Leu Ala Arg Ser Gln
 145 150 155 160
 Gly Arg Tyr Thr Thr Asp Asp Gly Tyr Ile Phe Asn Ala Ser Asp Ile
 165 170 175
 Ile Glu Asp Thr Gly Asp Ala Tyr Ile Val Pro His Gly Asp His Tyr
 180 185 190
 His Tyr Ile Pro Lys Asn Glu Leu Ser Ala Ser Glu Leu Ala Ala Ala
 195 200 205
 Glu Ala Phe Leu Ser Gly Arg Gly Asn Leu Ser Asn Ser Arg Thr Tyr
 210 215 220
 Arg Arg Gln Asn Ser Asp Asn Thr Ser Arg Thr Asn Trp Val Pro Ser
 225 230 235 240
 Val Ser Asn Pro Gly Thr Thr Asn Thr Asn Thr Ser Asn Asn Ser Asn
 245 250 255
 Thr Asn Ser Gln Ala Ser Gln Ser Asn Asp Ile Asp Ser Leu Leu Lys
 260 265 270
 Gln Leu Tyr Lys Leu Pro Leu Ser Gln Arg His Val Glu Ser Asp Gly
 275 280 285
 Leu Val Phe Asp Pro Ala Gln Ile Thr Ser Arg Thr Ala Arg Gly Val
 290 295 300
 Ala Val Pro His Gly Asp His Tyr His Phe Ile Pro Tyr Ser Gln Met
 305 310 315 320
 Ser Glu Leu Glu Glu Arg Ile Ala Arg Ile Ile Pro Leu Arg Tyr Arg
 325 330 335
 Ser Asn His Trp Val Pro Asp Ser Arg Pro Glu Gln Pro Ser Pro Gln

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340

345

350

Pro Thr Pro Glu Pro Ser Pro Gly Pro Gln Pro Ala Pro Asn Leu Lys
 355 360 365

Ile Asp Ser Asn Ser Ser Leu Val Ser Gln Leu Val Arg Lys Val Gly
 370 375 380

Glu Gly Tyr Val Phe Glu Glu Lys Gly Ile Ser Arg Tyr Val Phe Ala
 385 390 395 400

Lys Asp Leu Pro Ser Glu Thr Val Lys Asn Leu Glu Ser Lys Leu Ser
 405 410 415

Lys Gln Glu Ser Val Ser His Thr Leu Thr Ala Lys Lys Glu Asn Val
 420 425 430

Ala Pro Arg Asp Gln Glu Phe Tyr Asp Lys Ala Tyr Asn Leu Leu Thr
 435 440 445

Glu Ala His Lys Ala Leu Phe Xaa Asn Lys Gly Arg Asn Ser Asp Phe
 450 455 460

Gln Ala Leu Asp Lys Leu Leu Glu Arg Leu Asn Asp Glu Ser Thr Asn
 465 470 475 480

Lys Glu Lys Leu Val Asp Asp Leu Leu Ala Phe Leu Ala Pro Ile Thr
 485 490 495

His Pro Glu Arg Leu Gly Lys Pro Asn Ser Gln Ile Glu Tyr Thr Glu
 500 505 510

Asp Glu Val Arg Ile Ala Gln Leu Ala Asp Lys Tyr Thr Thr Ser Asp
 515 520 525

Gly Tyr Ile Phe Asp Glu His Asp Ile Ile Ser Asp Glu Gly Asp Ala
 530 535 540

Tyr Val Thr Pro His Met Gly His Ser His Trp Ile Gly Lys Asp Ser
 545 550 555 560

Leu Ser Asp Lys Glu Lys Val Ala Ala Gln Ala Tyr Thr Lys Glu Lys
 565 570 575

Gly Ile Leu Pro Pro Ser Pro Asp Ala Asp Val Lys Ala Asn Pro Thr
 580 585 590

Gly Asp Ser Ala Ala Ala Ile Tyr Asn Arg Val Lys Gly Glu Lys Arg
 595 600 605

Ile Pro Leu Val Arg Leu Pro Tyr Met Val Glu His Thr Val Glu Val
 610 615 620

Lys Asn Gly Asn Leu Ile Ile Pro His Lys Asp His Tyr His Asn Ile
 625 630 635 640

Lys Phe Ala Trp Phe Asp Asp His Thr Tyr Lys Ala Pro Asn Gly Tyr
 645 650 655

Thr Leu Glu Asp Leu Phe Ala Thr Ile Lys Tyr Tyr Val Glu His Pro
 660 665 670

Asp Glu Arg Pro His Ser Asn Asp Gly Trp Gly Asn Ala Ser Glu His

09765272.01201

675		680		685
Val Leu Gly Lys Lys Asp His Ser Glu Asp Pro Asn Lys Asn Phe Lys				
690		695		700
Ala Asp Glu Glu Pro Val Glu Glu Thr Pro Ala Glu Pro Glu Val Pro				
705		710		720
Gln Val Glu Thr Glu Lys Val Glu Ala Gln Leu Lys Glu Ala Glu Val				
	725		730	735
Leu Leu Ala Lys Val Thr Asp Ser Ser Leu Lys Ala Asn Ala Thr Glu				
	740		745	750
Thr Leu Ala Gly Leu Arg Asn Asn Leu Thr Leu Gln Ile Met Asp Asn				
	755		760	765
Asn Ser Ile Met Ala Glu Ala Glu Lys Leu Leu Ala Leu Leu Lys Gly				
	770		775	780
Ser Asn Pro Ser Ser Val Ser Lys Glu Lys Ile Asn				
	785		790	795

(2) INFORMATION FOR SEQ ID NO: 57:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1180 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

TACTGAGATG CATCATAATC TAGGAGCTGA AAAGCGTTCA GCAGTGGCTA CTACTATCGA	60
TAGTTTTAAG GAGCGAAGTC AAAAAGTCAG AGCACTATCT GATCCAAATG TCGTTTTTGT	120
TCCCTTCTTT GGCTCTAGTG AATGGCTTCG TTTTGACGGT GTCATTTCTG CGGTATTAGC	180
TGAGAATAC AATCGTTTCT ACCGTCCTTA TCTTTTAGGA CAGGGGGGAG CTGCATCGCT	240
TAACCAATAT TTTGGAATGC AACAGATGTT ACCACAGCTG GAGAATAAAC AAGTTGTGTA	300
TGTTATCTCA CCTCAGTGGT TCAGTAAAAA TGGCTATGAT CCAGCAGCCT TCCAGCAGTA	360
TTTTATGGA GACCAGTTGA CTAGTTTCTT GAAACATCAA TCTGGGGATC AGGCTAGTCA	420
ATATGCAGCG ACTCGCTTAC TGCAACAGTT CCCAACGTA GCTATGAAGG ACCTGGTTCA	480
GAAGTTGGCA AGTAAAGAAG AATTGTCGAC AGCAGACAAT GAAATGATTG AATTATTGGC	540
TCGTTTTAAT GAACGCCAAG CTCCTTTTTT TGGTCAGTTT TCGGTAGAG GCTATGTTAA	600
CTACGATAAG CATGTAGCTA AGTATTTAAA AATCTTGCCA GACCAGTTTT CTTATCAGGC	660
AATAGAAGAT GTTGTCAAAG CAGATGCTGA AAAAAACTT TCCAATAATG AGATGGGAAT	720
GGAAAATTAT TTCTATAATG AGCAGATCAA GAAGGATTGG AAGAAATTAA AGGATTCCTCA	780
GAAAAAGCTT ACCTATCTCA AGTCGCCAGA GTATAATGNN TTGCAAGTTG TTTTAACACA	840

GTTTTCTAAA TCTAAGGTAA ACCCGATTTT TATCATTCCA CCTGTTAATA AAAAATGGAT	900
GNACTATGCT GGTCTACGAG AGGATATGTA CCAACAAACG GTGCAGAAGA TCGCTACCA	960
GTTAGAAAGT CAAGGTTTTT CCAATATAGC AGATTTTCT AAGGACGGCG GGGAGCCTTT	1020
CTTTATGAAG GACACCATTC ACCTTGGTTG GTTGGGTGG TTGGCTTTTG ACAAGGCAGT	1080
TGATCCTTTC CTATCCAATC CCACACCAGC TCCGACTTAC CATCTGAATG AGCGCTTTT	1140
CAGCAAAGAT TGGGGGACTT ATGATGGAGA TGTCAAAGAA	1180

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 393 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Thr	Glu	Met	His	His	Asn	Leu	Gly	Ala	Glu	Lys	Arg	Ser	Ala	Val	Ala	1	5	10	15
Thr	Thr	Ile	Asp	Ser	Phe	Lys	Glu	Arg	Ser	Gln	Lys	Val	Arg	Ala	Leu	20	25	30	
Ser	Asp	Pro	Asn	Val	Arg	Phe	Val	Pro	Phe	Phe	Gly	Ser	Ser	Glu	Trp	35	40	45	
Leu	Arg	Phe	Asp	Gly	Ala	His	Ser	Ala	Val	Leu	Ala	Glu	Lys	Tyr	Asn	50	55	60	
Arg	Ser	Tyr	Arg	Pro	Tyr	Leu	Leu	Gly	Gln	Gly	Gly	Ala	Ala	Ser	Leu	65	70	75	80
Asn	Gln	Tyr	Phe	Gly	Met	Gln	Gln	Met	Leu	Pro	Gln	Leu	Glu	Asn	Lys	85	90	95	
Gln	Val	Val	Tyr	Val	Ile	Ser	Pro	Gln	Trp	Phe	Ser	Lys	Asn	Gly	Tyr	100	105	110	
Asp	Pro	Ala	Ala	Phe	Gln	Gln	Tyr	Phe	Asn	Gly	Asp	Gln	Leu	Thr	Ser	115	120	125	
Phe	Leu	Lys	His	Gln	Ser	Gly	Asp	Gln	Ala	Ser	Gln	Tyr	Ala	Ala	Thr	130	135	140	
Arg	Leu	Leu	Gln	Gln	Phe	Pro	Asn	Val	Ala	Met	Lys	Asp	Leu	Val	Gln	145	150	155	160
Lys	Leu	Ala	Ser	Lys	Glu	Glu	Leu	Ser	Thr	Ala	Asp	Asn	Glu	Met	Ile	165	170	175	
Glu	Leu	Leu	Ala	Arg	Phe	Asn	Glu	Arg	Gln	Ala	Ser	Phe	Phe	Gly	Gln	180	185	190	
Phe	Ser	Val	Arg	Gly	Tyr	Val	Asn	Tyr	Asp	Lys	His	Val	Ala	Lys	Tyr	195	200	205	

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Leu Lys Ile Leu Pro Asp Gln Phe Ser Tyr Gln Ala Ile Glu Asp Val
 210 215 220
 Val Lys Ala Asp Ala Glu Lys Asn Thr Ser Asn Asn Glu Met Gly Met
 225 230 235 240
 Glu Asn Tyr Phe Tyr Asn Glu Gln Ile Lys Lys Asp Leu Lys Lys Leu
 245 250 255
 Lys Asp Ser Gln Lys Ser Phe Thr Tyr Leu Lys Ser Pro Glu Tyr Asn
 260 265 270
 Xaa Leu Gln Leu Val Leu Thr Gln Phe Ser Lys Ser Lys Val Asn Pro
 275 280 285
 Ile Phe Ile Ile Pro Pro Val Asn Lys Lys Trp Met Xaa Tyr Ala Gly
 290 295 300
 Leu Arg Glu Asp Met Tyr Gln Gln Thr Val Gln Lys Ile Arg Tyr Gln
 305 310 315 320
 Leu Glu Ser Gln Gly Phe Thr Asn Ile Ala Asp Phe Ser Lys Asp Gly
 325 330 335
 Gly Glu Pro Phe Phe Met Lys Asp Thr Ile His Leu Gly Trp Leu Gly
 340 345 350
 Trp Leu Ala Phe Asp Lys Ala Val Asp Pro Phe Leu Ser Asn Pro Thr
 355 360 365
 Pro Ala Pro Thr Tyr His Leu Asn Glu Arg Phe Phe Ser Lys Asp Trp
 370 375 380
 Ala Thr Tyr Asp Gly Asp Val Lys Glu
 385 390

(2) INFORMATION FOR SEQ ID NO: 59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1423 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

GGTTTTGAGA AAGTATTGTC AGGGGGCCCT GATTGAGTCG ATTGAGCAAG TGGAAATGA 60
 CCGTATTGTG GAAATTACAG TTCCAATAA AAACGAGATT GGAGACCATA TCCAGGCTAC 120
 CTTGATTATC GAAATTATGG GGAACACAG TAATATICTA CTGGTCGATA AAAGCAGTCA 180
 TAAAACTCTC GAAGTTATCA AACACGTCGG CTTTTCACAA AATAGCTACC GCACCTTACT 240
 TCCAGGATCG ACCTATATCG CTCGCGCAAG TACAAAATCT CTCAATCCTT TTACTATCAA 300
 GGATGAAAAG CTCTTTGAAA TCCTGCAAAC CCAAGAACTA ACAGCAAAAA ATCTTCRAAG 360
 CCTCTTTCAA GGTCTGGGAC GCGATACGGC AAATGAATTG GAAAGGATAC TGGTTAGTGA 420

AAAACTTTCC GCTTTCCGAA ATTTTTTCAA TCAAGAAACC AAGCCATGCT TGA CTGAGAC 480
 TTCCTTCAGT CCASTTCCTT TTGCAAAATCA GGTGGGAGAG CCTTTTGCAA ATCTTTCTGA 540
 TTTGTTGGAC ACCTACTATA AGGATAAGGC TGAGCGCGAC CGCGTCAAAC AGCAGGCCAG 600
 TGAAGTATTG CGTCGTGTTG AAAATGAACT TCAGAAAAAC CGACACAAAC TCAAAAAACA 660
 GGAAAAAGAG TTACTGGCGA CAGACAACGC TGAAGAATTT CGTCAAAAAG GAGAATTGCT 720
 GACAACCTTC CTCCACCAAG TGCTTAACGA CCAAGACCAG GTTATCCTAG ACAACTACTA 780
 TACCAACCAA CCTATCATGA TTGCGCTTGA TAAGGCTCTG ACTCCCAACC AGAATGCCCA 840
 ACGCTATTTT AAACGGTATC AGAAACTCAA AGAAGCTGTC AAATACTTGA CTGATTGAT 900
 TGAAGAAACC AAAGCCACTA TTCTCTATCT GGAAAGTGTA GAAACCGTCC TCAACCAAGC 960
 TGGACTGGAA GAAATCGCTG AAATCCGTGA AGAATTGATT CAAACAGGTT TTATCCGCAG 1020
 AAGACAACGG GAGAAAATCC AGAAACGCAA AAAACTAGAA CAATATCTAG CAAGCGATGG 1080
 CAAACCATC ATCTATGTCG GACGAAACAA TCTTCAAAAT GAGGAATTGA CCTTTAAAAT 1140
 GGCCCGCAAG GAGGAACCTT GGTTCATGTC TAAGGACATT CCTGGAAGCC ATGTTGTCAT 1200
 CTCAGGAAT CTGACCCAT CTGATGCAGT CAAGACAGAC GCAGCAGAGT TAGCTGCCTA 1260
 CTCTCTCAAA GGGCGCTGT CGAATCTGGT GCAGGTAGAT ATGATTGAAG TCAAAAAACT 1320
 CAATAAACCA ACTGGTGGAA AACC CGGCTT TGTCACTTAC ACAGGACAAA AGACCTCCG 1380
 CGTCACACCA GACTCCAAAA AAATGTCATC CATGAAAAAA TCC 1423

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 474 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Val Leu Arg Lys Tyr Leu Gln Gly Ala Leu Ile Glu Ser Ile Glu Gln
 1 5 10 15
 Val Glu Asn Asp Arg Ile Val Glu Ile Thr Val Ser Asn Lys Asn Glu
 20 25 30
 Ile Gly Asp His Ile Gln Ala Thr Leu Ile Ile Glu Ile Met Gly Lys
 35 40 45
 His Ser Asn Ile Leu Leu Val Asp Lys Ser Ser His Lys Ile Leu Glu
 50 55 60
 Val Ile Lys His Val Gly Phe Ser Gln Asn Ser Tyr Arg Thr Leu Leu
 65 70 75 80
 Pro Gly Ser Thr Tyr Ile Ala Pro Pro Ser Thr Lys Ser Leu Asn Pro

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Phe	Thr	Ile	Lys	Asp	Glu	Lys	Leu	Phe	Glu	Ile	Leu	Gln	Thr	Gln	Glu	
		100						105					110			
Leu	Thr	Ala	Lys	Asn	Leu	Gln	Ser	Leu	Phe	Gln	Gly	Leu	Gly	Arg	Asp	
		115					120					125				
Thr	Ala	Asn	Glu	Leu	Glu	Arg	Ile	Leu	Val	Ser	Glu	Lys	Leu	Ser	Ala	
		130				135						140				
Phe	Arg	Asn	Phe	Phe	Asn	Gln	Glu	Thr	Lys	Pro	Cys	Leu	Thr	Glu	Thr	
		145			150					155					160	
Ser	Phe	Ser	Pro	Val	Pro	Phe	Ala	Asn	Gln	Val	Gly	Glu	Pro	Phe	Ala	
				165					170					175		
Asn	Leu	Ser	Asp	Leu	Leu	Asp	Thr	Tyr	Tyr	Lys	Asp	Lys	Ala	Glu	Arg	
			180					185					190			
Asp	Arg	Val	Lys	Gln	Gln	Ala	Ser	Glu	Leu	Ile	Arg	Arg	Val	Glu	Asn	
		195					200					205				
Glu	Leu	Gln	Lys	Asn	Arg	His	Lys	Leu	Lys	Lys	Gln	Glu	Lys	Glu	Leu	
		210				215					220					
Leu	Ala	Thr	Asp	Asn	Ala	Glu	Glu	Phe	Arg	Gln	Lys	Gly	Glu	Leu	Leu	
				230						235					240	
Thr	Thr	Phe	Leu	His	Gln	Val	Pro	Asn	Asp	Gln	Asp	Gln	Val	Ile	Leu	
				245					250					255		
Asp	Asn	Tyr	Tyr	Thr	Asn	Gln	Pro	Ile	Met	Ile	Ala	Leu	Asp	Lys	Ala	
			260					265					270			
Leu	Thr	Pro	Asn	Gln	Asn	Ala	Gln	Arg	Tyr	Phe	Lys	Arg	Tyr	Gln	Lys	
		275					280					285				
Leu	Lys	Glu	Ala	Val	Lys	Tyr	Leu	Thr	Asp	Leu	Ile	Glu	Glu	Thr	Lys	
		290				295					300					
Ala	Thr	Ile	Leu	Tyr	Leu	Glu	Ser	Val	Glu	Thr	Val	Leu	Asn	Gln	Ala	
					310					315					320	
Gly	Leu	Glu	Glu	Ile	Ala	Glu	Ile	Arg	Glu	Glu	Leu	Ile	Gln	Thr	Gly	
				325					330					335		
Phe	Ile	Arg	Arg	Arg	Gln	Arg	Glu	Lys	Ile	Gln	Lys	Arg	Lys	Lys	Leu	
			340					345					350			
Glu	Gln	Tyr	Leu	Ala	Ser	Asp	Gly	Lys	Thr	Ile	Ile	Tyr	Val	Gly	Arg	
		355					360					365				
Asn	Asn	Leu	Gln	Asn	Glu	Glu	Leu	Thr	Phe	Lys	Met	Ala	Arg	Lys	Glu	
						375					380					
Glu	Leu	Trp	Phe	His	Ala	Lys	Asp	Ile	Pro	Gly	Ser	His	Val	Val	Ile	
					390					395					400	
Ser	Gly	Asn	Leu	Asp	Pro	Ser	Asp	Ala	Val	Lys	Thr	Asp	Ala	Ala	Glu	
				405				410						415		
Leu	Ala	Ala	Tyr	Phe	Ser	Gln	Gly	Arg	Leu	Ser						

420

425

430

Asp Met Ile Glu Val Lys Lys Leu Asn Lys Pro Thr Gly Gly Lys Pro
435 440 445

Gly Phe Val Thr Tyr Thr Gly Gln Lys Thr Leu Arg Val Thr Pro Asp
450 455 460

Ser Lys Lys Ile Ala Ser Met Lys Lys Ser
465 470

(2) INFORMATION FOR SEQ ID NO: 61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 544 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

GACAAACATT	ACTATCCATA	CAGTAGAGTC	AGCACCAGCA	GAAGTGAAAG	AAATTCTTGA	60
AACAGTAGAA	AAAGACAACA	ATGGCTATAT	TCCCAACCTA	ATCGTCTCT	TGGCCAATGC	120
CCCGACTGTT	TTAGAAGCCT	ACCAAAATGT	CTCATCTATC	CACCGTCGCA	ACAGCCTGAC	180
ACCCGTTGAG	CGTGAAGTGG	TGCAAAATCAC	GGCAGCCGTG	ACCAATGGTT	GTGCCCTCTG	240
TGTCGACAGT	CACACAGCCT	TTTCCATCAA	ACAAATCCAG	ATGAATGATG	ACTTGATTCA	300
AGCTCTTCGC	AATCGTACTC	CAATTGAAAC	AGATCTCTAA	TTGGATACCC	TAGCTAAGTT	360
TACCTTGCCA	GTTATCAATA	CCAAGGGTCG	TGTAGGAGAT	GAAGCCTTGT	CTGAGTPTTT	420
AGAAGCTGGC	TACACTCAAC	AAAATGCCTT	GGATGTGGTT	TTTGGTGTC	GCCTAGCAAT	480
CCTCTGTAAC	TATGCCAACA	ACTTAGCTAA	TACACCAATT	AATCCAGAAT	TGCAACCTTA	540
TGCC						544

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 181 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Thr Thr Phe Thr Ile His Thr Val Glu Ser Ala Pro Ala Glu Val Lys
1 5 10 15

Glu Ile Leu Glu Thr Val Glu Lys Asp Asn Asn Gly Tyr Ile Pro Asn _____
20 25 30

Leu Ile Gly Leu Leu Ala Asn Ala Pro Thr Val Leu Glu Ala Tyr Gln

35		40		45
Ile Val Ser Ser Ile His Arg Arg Asn Ser Leu Thr Pro Val Glu Arg				
50		55	60	
Glu Val Val Gln Ile Thr Ala Ala Val Thr Asn Gly Cys Ala Phe Cys				
65	70	75	80	
Val Ala Gly His Thr Ala Phe Ser Ile Lys Gln Ile Gln Met Asn Asp				
	85	90	95	
Asp Leu Ile Gln Ala Leu Arg Asn Arg Thr Pro Ile Glu Thr Asp Pro				
	100	105	110	
Lys Leu Asp Thr Leu Ala Lys Phe Thr Leu Ala Val Ile Asn Thr Lys				
	115	120	125	
Gly Arg Val Gly Asp Glu Ala Leu Ser Glu Phe Leu Glu Ala Gly Tyr				
	130	135	140	
Thr Gln Gln Asn Ala Leu Asp Val Val Phe Gly Val Ser Leu Ala Ile				
	145	150	155	160
Leu Cys Asn Tyr Ala Asn Asn Leu Ala Asn Thr Pro Ile Asn Pro Glu				
	165	170	175	
Leu Gln Pro Tyr Ala				
	180			

(2) INFORMATION FOR SEQ ID NO: 63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 811 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

GGCTAAGGAA AGAGTGGATG TACTAGCTTA TAAACAGGGG TTGTTTGAAA CGAGAGAGCA	60
GGCCAAGCGA GGTGTGATGG CTGGCCTAGT CGTAGCAGTC CTTAATGGAG AACGGTTTGA	120
CAAGCCAGGA GAGAAATTC CAGATGACAC CGAATTAAAA CTCAAGGGGG AGAAACTCAA	180
GTATGTCAGC CGTGTGGTT TGAAGCTGGA AAAGGCCTTG CAGGTCCTTG ATTTGTCGGT	240
GGATGCGCGC ACTACGATTG ATATCGGGGC CTCTACTGGA GGTTTTACCG ATGCTCATGCT	300
ACAGAATAGT GCCAAGTTGG TCTTTGCAGT CGATGTTGGT ACCAATCAGT TGGCTTGGAA	360
ATTACGCCAA GACCACGAG TTGTCAGCAT GGAGCAGTTC AATTTCGCT ATGCTGAAAA	420
GACTGATTTT GAGCAGGAGC CGAGCTTTGC CAGTATTGAT GTGAGTTTCA TTTCCTTAG	480
TCTGATTTTG CCAGCCTTGC ACCGTGTCTT GGCTGATCAA GGTCAAGTGG TAGCACTTGT	540
CAAACCTCAG TTTGAGGCAG GACGTGAGCA GATTGGGAAA AATGGAATTA TTCGAGATGC	600
TAAGGTTTCA CAGAATGTCC TTGAATCTGT AACAGCTATG GCAGTAGAGG TAGGTTTTTC	660

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AGTCCTTGGC TTGGACTTTT CTCCCATCCA AGGTGGACAT GGAAATATG AATTTTATGC 720
 GTATTTGAAA AAAGAAAAGT CAGCAAGCAA TCAGATTCTT GCTGAGATTA AAGAAGCAGT 780
 AGAGAGGGCG CATAGTCAAT TAAAAATGA A 811

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Ala Lys Glu Arg Val Asp Val Leu Ala Tyr Lys Gln Gly Leu Phe Glu
 1 5 10 15
 Thr Arg Glu Gln Ala Lys Arg Gly Val Met Ala Gly Leu Val Val Ala
 20 25 30
 Val Leu Asn Gly Glu Arg Phe Asp Lys Pro Gly Glu Lys Ile Pro Asp
 35 40 45
 Asp Thr Glu Leu Lys Leu Lys Gly Glu Lys Leu Lys Tyr Val Ser Arg
 50 55 60
 Gly Gly Leu Lys Leu Glu Lys Ala Leu Gln Val Phe Asp Leu Ser Val
 65 70 75 80
 Asp Gly Ala Thr Thr Ile Asp Ile Gly Ala Ser Thr Gly Gly Phe Thr
 85 90 95
 Asp Val Met Leu Gln Asn Ser Ala Lys Leu Val Phe Ala Val Asp Val
 100 105 110
 Gly Thr Asn Gln Leu Ala Trp Lys Leu Arg Gln Asp Pro Arg Val Val
 115 120 125
 Ser Met Glu Gln Phe Asn Phe Arg Tyr Ala Glu Lys Thr Asp Phe Glu
 130 135 140
 Gln Glu Pro Ser Phe Ala Ser Ile Asp Val Ser Phe Ile Ser Leu Ser
 145 150 155 160
 Leu Ile Leu Pro Ala Leu His Arg Val Leu Ala Asp Gln Gly Gln Val
 165 170 175
 Val Ala Leu Val Lys Pro Gln Phe Glu Ala Gly Arg Glu Gln Ile Gly
 180 185 190
 Lys Asn Gly Ile Ile Arg Asp Ala Lys Val His Gln Asn Val Leu Glu
 195 200 205
 Ser Val Thr Ala Met Ala Val Glu Val Gly Phe Ser Val Leu Gly Leu
 210 215 220
 Asp Phe Ser Pro Ile Gln Gly Gly His Gly Asn Ile Glu Phe Leu Ala
 225 230 235 240

Tyr Leu Lys Lys Glu Lys Ser Ala Ser Asn Gln Ile Leu Ala Glu Ile
245 250 255

Lys Glu Ala Val Glu Arg Ala His Ser Gln Phe Lys Asn Glu
260 265 270

(2) INFORMATION FOR SEQ ID NO: 65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2290 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

TTGTTCCCTAT GAACCTTGGTC GTCACCAAGC TGTCAGGTT AAGAAAGAGT CTAATCGAGT	60
TTCTTATATA GATGTGATC AGGCTGGTCA AAAGGCAGAA AACTTGACAC CAGATGAAGT	120
CAGTAAGAGG GAGGGGATCA ACGCCGAACA AATNGTNATC AAGATTACGG ATCAAGGTTA	180
TGTGACCTCT CATGGAGACC ATTATCATT CTATAATGGC AAGGTTCCCT ATGATGCCAT	240
CATCAGTGAA GAGCTCCTCA TGAAGATCC GAATTATCAG TTGAAGGATT CAGACATTGT	300
CAATGAAATC AAGGGTGSTT ATGTCATTAA GGTAAACGCT AAATACTATG TNTACCTTAA	360
GGATGCAGCT CATGCGGATA ATATTTCGGAC AAAAGAAGAG ATTAAACGTC AGAAGCAGGA	420
ACGCAGTCAT AATCATAACT CAAGAGCAGA TAATGCTGTT GCTGCAGCCA GAGCCCAAGG	480
ACGTTATACA ACGGATGATG GGTATATCTT CAATGCATCT GATATCATTG AGGACACGGG	540
TGATGCTTAT ATCGTTCCCTC ACGGCGACCA TTACCATTAC ATTCCTAAGA ATGAGTTATC	600
AGCTAGCGAG TTAGTCGCTG CAGAAGCCTA TTGGAATGGG AAGCAGGGAT CTCGTCCTTC	660
TTCAAGTTCT AGTTATAATG CAAATCCAGC TCAACCAAGA TTGTCAGAGA ACCACAATCT	720
GACTGTCACT CCAACTTATC ATCAAAATCA AGGGGAAAAC ATTTCAAGCC TTTTACGTGA	780
ATTGTATGCT AAACCCCTTAT CAGAAGGCCA TGTGGAATCT GATGGCCTTA TTTTCGACCC	840
AGCGCAAACT ACAAGTCGAA CCGCCAGAGG TGTAGCTGTC CCTCATGGTA ACCATTACCA	900
CTTTATCCCT TATGAACAAA TGTCTGAATT GAAAAACGA ATTGCTCGTA TTATTCCCCT	960
TCGTTATCGT TCAAAACCATT GGGTACCAGA TTCAAGACCA GAACAACCAA GTCCACAATC	1020
GACTCCGGAA CCTAGTCCAA GTCCGCAACC TGCACCAAT CCTCAACCAAG CTCCAAGCAA	1080
TCCAATTGAT GAGAAATTGG TCAAAGAAGC TGTTCGAAAA GTAGGCGATG GTTATGTCTT	1140
TGAGGAGAAT GGAGTTTCTC GTTATATCCC AGCCAAGGAT CTTTCAGCAG AAACAGCAGC	1200
AGGCATTGAT AGCAAATCG CCAAGCAGGA AAGTTTATCT CATAAGCTAG GAGCTAAGAA	1260
AAC TGACCTC CCATCTAGTG ATCGAGAATT TTACAATAAG GCTTATGACT TACTAGCAAG	1320

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AATTCACCAA GATTACTTG ATAATAAAGG TCGACAAGTT GATTTTGAGG CTTTGATATA 1380
 CCTGTTGGAA CGACTCAAGG ATGTCNCAAG TGATAAAGTC AAGTTAGTGG ANGATATTCT 1440
 TGCCCTTCTTA GCTCCGATTC GTCATCCAGA ACGTTTAGGA AAACCAATG CGCAAAATTAC 1500
 CTCACTGAT GATGAGATTC AAGTAGCCAA GTTGGCAGCG AAGTACACAA CAGAAGACGG 1560
 TTATATCTTT GATCCTCGTG ATATAACCAG TGATGAGGGG GATGCCTATG TAACTCCACA 1620
 TATGACCAT AGCCACTGGA TTAATAAAGA TAGTTTGCTT GAAGCTGAGA GAGCGGCAGC 1680
 CCAGCCTTAT GCTAAAGAGA AAGSTTTGAC CCCTCCTTCG ACAGACCATC AGGATTGAGG 1740
 AAATACTGAG GCAAAAGGAG CAGAAGCTAT CTACACCGC GTGAAAGCAG CTAAGAAGGT 1800
 GCCACTTGAT CGTATGCCTT ACAATCTTCA ATATACTGTA GAAGTCAAAA ACGGTAGTTT 1860
 AATCATACCT CATTATGACC ATTACCATAA CATCAAATTT GAGTGGTTTG ACGAAGGCCT 1920
 TTATGAGGCA CCTAAGGGGT ATACTCTTGA GGATCTTTTG GCGACTGTCA AGTACTATGT 1980
 CGAACATCCA AACGAACGTC CGCATTGAGA TAATGGTTTT GGTACGCTA GCGACCATGT 2040
 TCAAAGAAAC AAAAATGGTC AAGCTGATAC CAATCAAACG GAAAAACCAA GCGAGGAGAA 2100
 ACCTCAGACA GAAAAACCTG AGGAAGAAAC CCCTCGAGAA GAGAAACCGC AAAGCGAGAA 2160
 ACCAGAGTCT CCAAACCAA CAGAGGAACC AGAAGAATCA CCAGAGGAAT CAGAAGAACC 2220
 TCAGGTCGAG ACTGAAAAGG TTGAAGAAAA ACTGAGAGAG GCTGAAGATT TACTTGGAAA 2280
 AATCCAGGAT 2290

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 763 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Cys Ser Tyr Glu Leu Gly Arg His Gln Ala Gly Gln Val Lys Lys Glu
 1 5 10 15
 Ser Asn Arg Val Ser Tyr Ile Asp Gly Asp Gln Ala Gly Gln Lys Ala
 20 25 30
 Glu Asn Leu Thr Pro Asp Glu Val Ser Lys Arg Glu Gly Ile Asn Ala
 35 40 45
 Glu Gln Xaa Val Ile Lys Ile Thr Asp Gln Gly Tyr Val Thr Ser His
 50 55 60
 Gly Asp His Tyr His Tyr Tyr Asn Gly Lys Val Pro Tyr Asp Ala Ile
 65 70 75 80
 Ile Ser Glu Glu Leu Leu Met Lys Asp Pro Asn Tyr Gln Leu Lys Asp

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Ser Asp Ile Val Asn Glu Ile Lys Gly Gly Tyr Val Ile Lys Val Asn
 100 105 110
 Gly Lys Tyr Tyr Val Tyr Leu Lys Asp Ala Ala His Ala Asp Asn Ile
 115 120 125
 Arg Thr Lys Glu Glu Ile Lys Arg Gln Lys Gln Glu Arg Ser His Asn
 130 135 140
 His Asn Ser Arg Ala Asp Asn Ala Val Ala Ala Arg Ala Gln Gly
 145 150 155 160
 Arg Tyr Thr Thr Asp Asp Gly Tyr Ile Phe Asn Ala Ser Asp Ile Ile
 165 170 175
 Glu Asp Thr Gly Asp Ala Tyr Ile Val Pro His Gly Asp His Tyr His
 180 185 190
 Tyr Ile Pro Lys Asn Glu Leu Ser Ala Ser Glu Leu Ala Ala Glu
 195 200 205
 Ala Tyr Trp Asn Gly Lys Gln Gly Ser Arg Pro Ser Ser Ser Ser
 210 215 220
 Tyr Asn Ala Asn Pro Ala Gln Pro Arg Leu Ser Glu Asn His Asn Leu
 225 230 235 240
 Thr Val Thr Pro Thr Tyr His Gln Asn Gln Gly Glu Asn Ile Ser Ser
 245 250 255
 Leu Leu Arg Glu Leu Tyr Ala Lys Pro Leu Ser Glu Arg His Val Glu
 260 265 270
 Ser Asp Gly Leu Ile Phe Asp Pro Ala Gln Ile Thr Ser Arg Thr Ala
 275 280 285
 Arg Gly Val Ala Val Pro His Gly Asn His Tyr His Phe Ile Pro Tyr
 290 295 300
 Glu Gln Met Ser Glu Leu Glu Lys Arg Ile Ala Arg Ile Ile Pro Leu
 305 310 315 320
 Arg Tyr Arg Ser Asn His Trp Val Pro Asp Ser Arg Pro Glu Gln Pro
 325 330 335
 Ser Pro Gln Ser Thr Pro Glu Pro Ser Pro Ser Pro Gln Pro Ala Pro
 340 345 350
 Asn Pro Gln Pro Ala Pro Ser Asn Pro Ile Asp Glu Lys Leu Val Lys
 355 360 365
 Glu Ala Val Arg Lys Val Gly Asp Gly Tyr Val Phe Glu Glu Asn Gly
 370 375 380
 Val Ser Arg Tyr Ile Pro Ala Lys Asp Leu Ser Ala Glu Thr Ala Ala
 385 390 395 400
 Gly Ile Asp Ser Lys Leu Ala Lys Gln Glu Ser Leu Ser His Lys Leu
 405 410 415
 Gly Ala Lys Lys Thr Asp Leu Pro Ser Ser Asp Arg Glu Phe Tyr Asn

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430

Lys Ala Tyr Asp Leu Leu Ala Arg Ile His Gln Asp Leu Leu Asp Asn
435 440 445

Lys Gly Arg Gln Val Asp Phe Glu Ala Leu Asp Asn Leu Leu Glu Arg
450 455 460

Leu Lys Asp Val Xaa Ser Asp Lys Val Lys Leu Val Xaa Asp Ile Leu
465 470 475 480

Ala Phe Leu Ala Pro Ile Arg His Pro Glu Arg Leu Gly Lys Pro Asn
485 490 495

Ala Gln Ile Thr Tyr Thr Asp Asp Glu Ile Gln Val Ala Lys Leu Ala
500 505 510

Gly Lys Tyr Thr Thr Glu Asp Gly Tyr Ile Phe Asp Pro Arg Asp Ile
515 520 525

Thr Ser Asp Glu Gly Asp Ala Tyr Val Thr Pro His Met Thr His Ser
530 535 540

His Trp Ile Lys Lys Asp Ser Leu Ser Glu Ala Glu Arg Ala Ala Ala
545 550 555 560

Gln Ala Tyr Ala Lys Glu Lys Gly Leu Thr Pro Pro Ser Thr Asp His
565 570 575

Gln Asp Ser Gly Asn Thr Glu Ala Lys Gly Ala Glu Ala Ile Tyr Asn
580 585 590

Arg Val Lys Ala Ala Lys Lys Val Pro Leu Asp Arg Met Pro Tyr Asn
595 600 605

Leu Gln Tyr Thr Val Glu Val Lys Asn Gly Ser Leu Ile Ile Pro His
610 615 620

Tyr Asp His Tyr His Asn Ile Lys Phe Glu Trp Phe Asp Glu Gly Leu
625 630 635 640

Tyr Glu Ala Pro Lys Gly Tyr Thr Leu Glu Asp Leu Leu Ala Thr Val
645 650 655

Lys Tyr Tyr Val Glu His Pro Asn Glu Arg Pro His Ser Asp Asn Gly
660 665 670

Phe Gly Asn Ala Ser Asp His Val Gln Arg Asn Lys Asn Gly Gln Ala
675 680 685

Asp Thr Asn Gln Thr Glu Lys Pro Ser Glu Glu Lys Pro Gln Thr Glu
690 695 700

Lys Pro Glu Glu Glu Thr Pro Arg Glu Glu Lys Pro Gln Ser Glu Lys
705 710 715 720

Pro Glu Ser Pro Lys Pro Thr Glu Glu Pro Glu Glu Ser Pro Glu Glu
725 730 735

Ser Glu Glu Pro Gln Val Glu Thr Glu Lys Val Glu Glu Lys Leu Arg
740 745 750

Glu Ala Glu Asp Leu Leu Gly Lys Ile Gln Asp

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(2) INFORMATION FOR SEQ ID NO: 67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

TTATAAGGGT	GAATTAGAAA	AAGGATACCA	ATTGTATGGT	TGGGAAATTT	CTGTTTTCGA	60
AGGTAAAAAA	GACGCTGGCT	ATGTTATTAA	TCTATCAAAA	GATACCTTTA	TAAAACCTGT	120
ATTCAAGAAA	ATAGAGGAGA	AAAAGGAGGA	AGAAAAATAA	CCTACTTTTG	ATGTATCGAA	180
AAAGAAAGAT	AACCCACAAG	TAAACCATAG	TCAATTAAAT	GAAAGTCACA	GAAAAGAGGA	240
TTTACAAAGA	GAAGAGCATT	CACAAAAATC	TGATTCAACT	AAGGATGTTA	CAGCTACAGT	300
TCTGTATAAA	AACAATATCA	GTAGTAAATC	AACCTACTAC	AATCCTAATA	AG	352

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

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Tyr  Lys  Gly  Glu  Leu  Glu  Lys  Gly  Tyr  Gln  Phe  Asp  Gly  Trp  Glu  Ile
1      5      10      15

Ser  Gly  Phe  Glu  Gly  Lys  Lys  Asp  Ala  Gly  Tyr  Val  Ile  Asn  Leu  Ser
20      25

Lys  Asp  Thr  Phe  Ile  Lys  Pro  Val  Phe  Lys  Lys  Ile  Glu  Glu  Lys  Lys
35      40      45

Glu  Glu  Glu  Asn  Lys  Pro  Thr  Phe  Asp  Val  Ser  Lys  Lys  Asp  Asn
50      55      60

Pro  Gln  Val  Asn  His  Ser  Gln  Leu  Asn  Glu  Ser  His  Arg  Lys  Glu  Asp
65      70      75      80

Leu  Gln  Arg  Glu  Glu  His  Ser  Gln  Lys  Ser  Asp  Ser  Thr  Lys  Asp  Val
85      90      95

Thr  Ala  Thr  Val  Leu  Asp  Lys  Asn  Asn  Ile  Ser  Ser  Lys  Ser  Thr  Thr
100     105     110

Asn  Asn  Pro  Asn  Lys
115

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(2) INFORMATION FOR SEQ ID NO: 69:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1312 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

GAATGTTGAG GCTCAAGAAA GTTCAGGAAA TAAATCCAC TTTATCAATG TTCAAGAAGG	60
TGGCAGTGAT GCGATTATTC TTGAAAGCAA TGGACATTTT GCCATGGTGG ATACAGGAGA	120
AGATTATGAT TTCCAGATG GAAGTGATTC TCGCTATCCA TGGAGAGAAG GAATTGAAAC	180
GTCTTATAAG CATGTTCTAA CAGACCGTGT CTTTCGTCGT TTGAAGGAAT TGGGTGTCCA	240
AAAACCTGAT TTTATTTTGG TGACCCATAC CCACAGTGAT CATATTGGAA ATGTTGATGA	300
ATTACTGTCT ACCTATCCAG TTGACCGAGT CTATCTTAAG AAATATAGTG ATAGTCGTAT	360
TACTAATCTT GAACGTCTAT GGGATAATCT GTATGGCTAT GATAAGGTTT TACAGACTGC	420
TGCAGAAAAA GGTGTTTCAG TTATTCAAAA TATCACAAA GGGGATGCTC ATTTTCAGTT	480
TGGGGACATG GATATTCAGC TGTATAATTA TGAAAATGAA ACTGATTCAT CGGGTGAATT	540
AAAGAAAAAT TGGGATGACA ATTCCAAATTC CTTGATTAGC GTGGTGAAAG TCAATGGCAA	600
GAAAATTTCAT CTGGGGGCGC ATTTAGATAA TGTTCATGGA GCAGAAGACA AGTATGGTCC	660
TCTCATGGA AAAAGTTGATT TGATGAAGTT TAATCATCAC CATGATACCA ACAAATCAAA	720
TACCAAGGAT TTCATTAAAA ATTTGAGTCC GAGTTTGATT GTTCAAACCT CGGATAGTCT	780
ACCTTGGAAA AATGTTGTTG ATAGTGAGTA TGTTAATTGG CTCAAAAGAAC GAGGAATTGA	840
GAGAAATCAAC GCAGCCAGCA AAGACTATGA TGCAACAGTT TTTGATATTC GAAAAGACGG	900
TTTTGTCAAT ATTTCAACAT CCTACAAGCC GATTCCAAGT TTTCAAGCTG GTTGGCATAA	960
GAGTGATAT GGGAACTGGT GGTATCAAGC GCCTGATTCT ACAGGAGAGT ATGCTGTCGG	1020
TTGGAATGAA ATCGAAGGTG AATGGTATTA CTTTAACCAA ACGGGTATCT TGTACAGAA	1080
TCAATGGAAA AAATGGAACA ATCATTGGTT CTATTTGACA GACTCTGGTG CTCTGCTAA	1140
AAATTGGAAG AAAATCGCTG GAATCTGGTA TTATTTTAAAC AAAGAAAACC AGATGGAAT	1200
TGGTTGGATT CAAGATAAAG AGCAGTGGTA TTATTTGGAT GTTGATGGTT CTATGAAGAC	1260
AGGATGGCTT CAATATATGG GGCAATGGTA TTACTTTGCT CCATCAGGGG AA	1312

(2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 437 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

```

Asn Val Gln Ala Gln Glu Ser Ser Gly Asn Lys Ile His Phe Ile Asn
 1           5           10           15

Val Gln Glu Gly Gly Ser Asp Ala Ile Ile Leu Glu Ser Asn Gly His
 20           25           30

Phe Ala Met Val Asp Thr Gly Glu Asp Tyr Asp Phe Pro Asp Gly Ser
 35           40           45

Asp Ser Arg Tyr Pro Trp Arg Glu Gly Ile Glu Thr Ser Tyr Lys His
 50           55           60

Val Leu Thr Asp Arg Val Phe Arg Arg Leu Lys Glu Leu Gly Val Gln
 65           70           75           80

Lys Leu Asp Phe Ile Leu Val Thr His Thr His Ser Asp His Ile Gly
 85           90           95

Asn Val Asp Glu Leu Leu Ser Thr Tyr Pro Val Asp Arg Val Tyr Leu
100           105           110

Lys Lys Tyr Ser Asp Ser Arg Ile Thr Asn Ser Glu Arg Leu Trp Asp
115           120           125

Asn Leu Tyr Gly Tyr Asp Lys Val Leu Gln Thr Ala Ala Glu Lys Gly
130           135           140

Val Ser Val Ile Gln Asn Ile Thr Gln Gly Asp Ala His Phe Gln Phe
145           150           155           160

Gly Asp Met Asp Ile Gln Leu Tyr Asn Tyr Glu Asn Glu Thr Asp Ser
165           170           175

Ser Gly Glu Leu Lys Lys Ile Trp Asp Asp Asn Ser Asn Ser Leu Ile
180           185           190

Ser Val Val Lys Val Asn Gly Lys Lys Ile Tyr Leu Gly Gly Asp Leu
195           200           205

Asp Asn Val His Gly Ala Glu Asp Lys Tyr Gly Pro Leu Ile Gly Lys
210           215           220

Val Asp Leu Met Lys Phe Asn His His His Asp Thr Asn Lys Ser Asn
225           230           235           240

Thr Lys Asp Phe Ile Lys Asn Leu Ser Pro Ser Leu Ile Val Gln Thr
245           250           255

Ser Asp Ser Leu Pro Trp Lys Asn Gly Val Asp Ser Glu Tyr Val Asn
260           265           270

Trp Leu Lys Glu Arg Gly Ile Glu Arg Ile Asn Ala Ala Ser Lys Asp
275           280           285

Tyr Asp Ala Thr Val Phe Asp Ile Arg Lys Asp Gly Phe Val Asn Ile
290           295           300

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Ser Thr Ser Tyr Lys Pro Ile Pro Ser Phe Gln Ala Gly Trp His Lys
305 310 315 320

Ser Ala Tyr Gly Asn Trp Trp Tyr Gln Ala Pro Asp Ser Thr Gly Glu
325 330 335

Tyr Ala Val Gly Trp Asn Glu Ile Glu Gly Glu Trp Tyr Tyr Phe Asn
340 345 350

Gln Thr Gly Ile Leu Leu Gln Asn Gln Trp Lys Lys Trp Asn Asn His
355 360 365

Trp Phe Tyr Leu Thr Asp Ser Gly Ala Ser Ala Lys Asn Trp Lys Lys
370 375 380

Ile Ala Gly Ile Trp Tyr Tyr Phe Asn Lys Glu Asn Gln Met Glu Ile
385 390 395 400

Gly Trp Ile Gln Asp Lys Glu Gln Trp Tyr Tyr Leu Asp Val Asp Gly
405 410 415

Ser Met Lys Thr Gly Trp Leu Gln Tyr Met Gly Gln Trp Tyr Tyr Phe
420 425 430

Ala Pro Ser Gly Glu
435

(2) INFORMATION FOR SEQ ID NO: 71:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1855 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

CTTGGGTGTA ACCCATATCC AGCTCCTTCC AGTCTTGTC TACTACTTTG TCAATGAATT 60

GAAAAACCAT GAACGCTTGT CTGACTACGC TTCAAGCAAC AGCAACTACA ACTGGGGATA 120

TGACCCTCAA AACTACTTCT CCTTGACTGG TATGTACTCA AGCGATCCTA AGAATCCAGA 180

AAAACGAATC GCAGAATTTA AAAACCTCAT CAACGAAATC CACAAACGTG GTATGGGAGC 240

TATCCTAGAT GTCGTTTATA ACCACACAGC CAAAGTCGAT CTCCTTTGAAG ATTTGGAACC 300

AAACTACTAC CACTTTATGG ATGCCGATGG CACACCTCGA ACTAGCTTTG GTGTGGGACG 360

CTTGGGGACA ACCCACCATA TGACCAAACG GCTCCTAATT GACTCTATCA AATACCTAGT 420

TGATACCTAC AAAGTGGATG GCTTCCGTTT CGATATGATG GGAGACCATG ACGCCGCTTC 480

TATCGAAGAA GCTTACAAGG CTGCACGCGC CCTCAATCCA AACCTCATCA TGCTTGGTGA 540

AGGTTGGAGA ACCTATGCCG GTGATGAAAA CATGCCTACT AAAGCTGCTG ACCAAGATTG 600

GATGAAACAT ACCGATACTG TCGCTGTCTT TTCAGATGAC ATCCGTAACA ACCTCAAATC 660

TGTTTATCCA AACGAAGGTC AACCTGCCTT TATCACAGGT GGCAAGCGTG ATGTCAACAC 720

CATCTTTAAA AATCTCATTG CTCAACCAAC TAACCTTTGAA GCTGACAGCC CTGGAGATGT 780
 CATCCAATAC ATCGCAGGCC ATGATAACTT GACCCTCTTT GACATCATTG CCCAGTCTAT 840
 CAAAAAGAC CCAAGCAAGG CTGAGAATA TGTGAAATC CACCGTCGTT TACGACTTGG 900
 AAATCTCATG GTCTTGACAG CTCAAGGAAC TCCATTATC CACTCCGGTC AGGAATATGG 960
 ACGTACTAAA CAATTCCGTG ACCCAGCCTA CAAGACTCCA GTAGCAGAG ATAAGSTTCC 1020
 AAACAAATCT CACTTGTGTC GTGATAAGGA CGGCAACCCA TTTGACTATC CTTACTTCAT 1080
 CCATGACTCT TACGATTCTA GTGATGCAGT CAACAAGTTT GACTGGACTA AGGCTACAGA 1140
 TGGTAAAGCT TATCCTGAAA ATGTCAAGAG CCGTGACTAT ATGAAAGGTT TGATTGCCCT 1200
 TCGTCAATCT ACAGATGCCT TCCGACTTAA GAGTCTTCAA GATATCAAAG ACCGTGTCCA 1260
 CCTCATCACT GTCCCAGGCC AAAATGGTGT GGAAAAAGAG GATGTAGTGA TTGGCTACCA 1320
 AATCACTGCT CCAACGCGG ATATCTACGC AGTCTTTGTC AATGCGGATG AAAAAGCTCG 1380
 CGAATTTAAT TTGGGAAGTC CCTTTGCACA TCTAAGAAAT GCGGAAGTTT TGSCAGATGA 1440
 AAACCAAGCA GGACCAAGTC GAATTGCCAA CCGGAAAGGA CTTGAATGGA CTGAAAAAGG 1500
 CTTGAAATTG AATGCCCTTA CAGCTACTGT TCTTCGAGTC TCTCAAAATG GAACTAGCCA 1560
 TGAGTCAACT GCAGAAGAGA AACCAGACTC AACCCTTCC AAGCCTGAAC ATCAAAATGA 1620
 AGCTTCTCAC CCTGCACATC AAGACCCAGC TCCAGAAGCT AGACCTGATT CTACTAAAC 1680
 AGATGCCAAA GTAGCTGATG CGGAAAAATA ACCTAGCCAA GCTACAGCTG ATTACAAGC 1740
 TGAACAACCA GCACAAGAAG CACAAGCATC ATCTGTAATA GAAGCGGTTT GAAACGAATC 1800
 GGTAGAAAAC TCTAGCAAGG AAAATATACC TGCAACCCCA GATAACAAG CTGAA 1855

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 618 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Leu Gly Val Thr His Ile Gln Leu Leu Pro Val Leu Ser Tyr Tyr Phe
 1 5 10 15
 Val Asn Glu Leu Lys Asn His Glu Arg Leu Ser Asp Tyr Ala Ser Ser
 20 25 30
 Asn Ser Asn Tyr Asn Trp Gly Tyr Asp Pro Gln Asn Tyr Phe Ser Leu
 35 40 45
 Thr Gly Met Tyr Ser Ser Asp Pro Lys Asn Pro Glu Lys Arg Ile Ala
 50 55 60

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Glu	Phe	Lys	Asn	Leu	Ile	Asn	Glu	Ile	His	Lys	Arg	Gly	Met	Gly	Ala	65	70	75	80
Ile	Leu	Asp	Val	Val	Tyr	Asn	His	Thr	Ala	Lys	Val	Asp	Leu	Phe	Glu	85	90	95	
Asp	Leu	Glu	Pro	Asn	Tyr	Tyr	His	Phe	Met	Asp	Ala	Asp	Gly	Thr	Pro	100	105	110	
Arg	Thr	Ser	Phe	Gly	Gly	Gly	Arg	Leu	Gly	Thr	Thr	His	His	Met	Thr	115	120	125	
Lys	Arg	Leu	Leu	Ile	Asp	Ser	Ile	Lys	Tyr	Leu	Val	Asp	Thr	Tyr	Lys	130	135	140	
Val	Asp	Gly	Phe	Arg	Phe	Asp	Met	Met	Gly	Asp	His	Asp	Ala	Ala	Ser	145	150	155	160
Ile	Glu	Glu	Ala	Tyr	Lys	Ala	Ala	Arg	Ala	Leu	Asn	Pro	Asn	Leu	Ile	165	170	175	
Met	Leu	Gly	Glu	Gly	Trp	Arg	Thr	Tyr	Ala	Gly	Asp	Glu	Asn	Met	Pro	180	185	190	
Thr	Lys	Ala	Ala	Asp	Gln	Asp	Trp	Met	Lys	His	Thr	Asp	Thr	Val	Ala	195	200	205	
Val	Phe	Ser	Asp	Asp	Ile	Arg	Asn	Asn	Leu	Lys	Ser	Gly	Tyr	Pro	Asn	210	215	220	
Glu	Gly	Gln	Pro	Ala	Phe	Ile	Thr	Gly	Gly	Lys	Arg	Asp	Val	Asn	Thr	225	230	235	240
Ile	Phe	Lys	Asn	Leu	Ile	Ala	Gln	Pro	Thr	Asn	Phe	Glu	Ala	Asp	Ser	245	250	255	
Pro	Gly	Asp	Val	Ile	Gln	Tyr	Ile	Ala	Ala	His	Asp	Asn	Leu	Thr	Leu	260	265	270	
Phe	Asp	Ile	Ile	Ala	Gln	Ser	Ile	Lys	Lys	Asp	Pro	Ser	Lys	Ala	Glu	275	280	285	
Asn	Tyr	Ala	Glu	Ile	His	Arg	Arg	Leu	Arg	Leu	Gly	Asn	Leu	Met	Val	290	295	300	
Leu	Thr	Ala	Gln	Gly	Thr	Pro	Phe	Ile	His	Ser	Gly	Gln	Glu	Tyr	Gly	305	310	315	320
Arg	Thr	Lys	Gln	Phe	Arg	Asp	Pro	Ala	Tyr	Lys	Thr	Pro	Val	Ala	Glu	325	330	335	
Asp	Lys	Val	Pro	Asn	Lys	Ser	His	Leu	Leu	Arg	Asp	Lys	Asp	Gly	Asn	340	345	350	
Pro	Phe	Asp	Tyr	Pro	Tyr	Phe	Ile	His	Asp	Ser	Tyr	Asp	Ser	Ser	Asp	355	360	365	
Ala	Val	Asn	Lys	Phe	Asp	Trp	Thr	Lys	Ala	Thr	Asp	Gly	Lys	Ala	Tyr	370	375	380	
Pro	Glu	Asn	Val	Lys	Ser	Arg	Asp	Tyr	Met	Lys	Gly	Leu	Ile	Ala	Leu	385	390	395	400

Arg Gln Ser Thr Asp Ala Phe Arg Leu Lys Ser Leu Gln Asp Ile Lys
405 410 415

Asp Arg Val His Leu Ile Thr Val Pro Gly Gln Asn Gly Val Glu Lys
420 425 430

Glu Asp Val Val Ile Gly Tyr Gln Ile Thr Ala Pro Asn Gly Asp Ile
435 440 445

Tyr Ala Val Phe Val Asn Ala Asp Glu Lys Ala Arg Glu Phe Asn Leu
450 455 460

Gly Thr Ala Phe Ala His Leu Arg Asn Ala Glu Val Leu Ala Asp Glu
465 470 475 480

Asn Gln Ala Gly Pro Val Gly Ile Ala Asn Pro Lys Gly Leu Glu Trp
485 490 495

Thr Glu Lys Gly Leu Lys Leu Asn Ala Leu Thr Ala Thr Val Leu Arg
500 505 510

Val Ser Gln Asn Gly Thr Ser His Glu Ser Thr Ala Glu Glu Lys Pro
515 520 525

Asp Ser Thr Pro Ser Lys Pro Glu His Gln Asn Glu Ala Ser His Pro
530 535 540

Ala His Gln Asp Pro Ala Pro Glu Ala Arg Pro Asp Ser Thr Lys Pro
545 550 555 560

Asp Ala Lys Val Ala Asp Ala Glu Asn Lys Pro Ser Gln Ala Thr Ala
565 570 575

Asp Ser Gln Ala Glu Gln Pro Ala Gln Glu Ala Gln Ala Ser Ser Val
580 585 590

Lys Glu Ala Val Arg Asn Glu Ser Val Glu Asn Ser Ser Lys Glu Asn
595 600 605

Ile Pro Ala Thr Pro Asp Lys Gln Ala Glu
610 615

(2) INFORMATION FOR SEQ ID NO: 73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1774 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

TAGTGATGGT ACTTGGCAAG GAAAACAGTA TCTGAAGAA GATGGCAGTC AAGCAGCAA	60
TGAGTGGGTT TTNGATACTC ATTATCAATC TIGGTTCTAT ATAAAGCAG ATGCTAACTA	120
TGCTGAAAAT GAATGGCTAA AGCAAGTGA CGACTATTTT TACCTCAAAT CTGGTGGCTA	180
TATGGCCAAA TCAGAAATGGG TAGAAGACAA GGGAGCCTTT TATTATCTTG ACCAAGATGG	240
AAAGATGAAA AGAAATGCTT GGGTAGGAAC TTCCTATGTT GGTGCAACAG GTGCCAAAGT	300

AATAGAAGAC TGGGTCTATG ATTCTCAATA CGATGCTTGG TTTTATATCA AAGCAGATGG 360
 ACAGCACGCA GAGAAAGAAT GGCTCCAAAT TAAAGGGAAG GACTATTATT TCAAATCCGG 420
 TGGTTATCTA CTGACAAGTC AGTGGATTAA TCAAGCTTAT GTGAATGCTA GTGGTGCCAA 480
 AGTACAGCAA GGTGGGCTTT TTGACAAACA ATACCAATCT TGGTTTTACA TCAAAGAAAA 540
 TGGAAACTAT GCTGATAAAG AATGGATTTT CGAGAATGGT CACTATTATT ATCTAAAAATC 600
 CGGTGGCTAC ATGGCAGCCA ATGAATGGAT TTGGGATAAG GAATCTTGGT TTTATCTCAA 660
 ATTTGATGGG AAAATGGCTG AAAAAGAATG GGTCTACGAT TCTCATAGTC AAGCTTGGTA 720
 CTACTTCAAA TCCGTTGGTT ACATGACAGC CAATGAATGG ATTTGGGATA AGGAATCTTG 780
 GTTTTACCTC AAATCTGATG GGAATAAGTC TGAATAAGAA TGGGTCTACG ATTTCTCATAG 840
 TCAAGCTTGG TACTACTTCA AATCTGGTGG CTACATGGCG AAAAATGAGA CAGTAGATGG 900
 TTATCAGCTT GGAAGCGATG GTAAATGGCT TGGAGGAAAA ACTACAAATG AAAATGCTGC 960
 TTACTATCAA GTAGTGCCCTG TTACAGCCAA TGTTTATGAT TCAGATGGTG AAAAGCTTTC 1020
 CTATATATCG CAAGTAGTGT TCGTATGGCT AGATAAGGAT AGAAAAAGTG ATGACAAGCG 1080
 CTTGGCTATT ACTATTCTGT GTTTGTCAGG CTATATGAAA ACAGAAGATT TACAAGCGCT 1140
 AGATGCTAGT AAGGACTTTA TCCCTTATTA TGAGAGTGAT GGCCACCGTT TTTATCACTA 1200
 TGTGGCTCAG AATGCTAGTA TCCAGTAGC TTCTCATCTT TCTGATATGG AAGTAGGCAA 1260
 GAAATATTAT TCGGCAGATG GCCTGCATTT TGATGGTTTT AAGCTTGAGA ATCCCTTCCT 1320
 TTTCAAAGAT TTAACAGAGG CTACAAACTA CAGTGTGAA GAATTGGATA AGGTATTTAG 1380
 TTTGCTAAAC ATTAACAATA GCCTTTTGGA GAACAAGGGC GCTACTTTTA AGGAAGCCGA 1440
 AGAACATTAC CATATCAATG CTCTTTATCT CCTTGCCCAT AGTGCCCTAG AAGTAAGTGT 1500
 GGGAGAAGT AAAATTGCCA AAGATAAGAA TAATTTCTTT GGCATTACAG CCTATGATAC 1560
 GACCCCTTAC CTTTCTGCTA AGACATTGTA TGATGTGGAT AAGGGAATTT TAGGTGCAAC 1620
 CAAGTGGATT AAGGAAAATT ATATCGATAG GGAAGAAGT TTCCTTGAA ACAAGGCTTC 1680
 TGGTATGAAT GTGGAATATG CTTGAGACCC TTATTGGGGC GAAAAAATG CTAGTGTGAT 1740
 GATGAAATC AATGAGAAGC TAGGTGGCAA AGAT 1774

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 591 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Ser Asp Gly Thr Trp Gln Gly Lys Gln Tyr Leu Lys Glu Asp Gly Ser
 1 5 10 15
 Gln Ala Ala Asn Glu Trp Val Xaa Asp Thr His Tyr Gln Ser Trp Phe
 20 25 30
 Tyr Ile Lys Ala Asp Ala Asn Tyr Ala Glu Asn Glu Trp Leu Lys Gln
 35 40 45
 Gly Asp Asp Tyr Phe Tyr Leu Lys Ser Gly Gly Tyr Met Ala Lys Ser
 50 55 60
 Glu Trp Val Glu Asp Lys Gly Ala Phe Tyr Tyr Leu Asp Gln Asp Gly
 65 70 75 80
 Lys Met Lys Arg Asn Ala Trp Val Gly Thr Ser Tyr Val Gly Ala Thr
 85 90 95
 Gly Ala Lys Val Ile Glu Asp Trp Val Tyr Asp Ser Gln Tyr Asp Ala
 100 105 110
 Trp Phe Tyr Ile Lys Ala Asp Gly Gln His Ala Glu Lys Glu Trp Leu
 115 120 125
 Gln Ile Lys Gly Lys Asp Tyr Tyr Phe Lys Ser Gly Gly Tyr Leu Leu
 130 135 140
 Thr Ser Gln Trp Ile Asn Gln Ala Tyr Val Asn Ala Ser Gly Ala Lys
 145 150 155 160
 Val Gln Gln Gly Trp Leu Phe Asp Lys Gln Tyr Gln Ser Trp Phe Tyr
 165 170 175
 Ile Lys Glu Asn Gly Asn Tyr Ala Asp Lys Glu Trp Ile Phe Glu Asn
 180 185 190
 Gly His Tyr Tyr Tyr Leu Lys Ser Gly Gly Tyr Met Ala Ala Asn Glu
 195 200 205
 Trp Ile Trp Asp Lys Glu Ser Trp Phe Tyr Leu Lys Phe Asp Gly Lys
 210 215 220
 Met Ala Glu Lys Glu Trp Val Tyr Asp Ser His Ser Gln Ala Trp Tyr
 225 230 235 240
 Tyr Phe Lys Ser Gly Gly Tyr Met Thr Ala Asn Glu Trp Ile Trp Asp
 245 250 255
 Lys Glu Ser Trp Phe Tyr Leu Lys Ser Asp Gly Lys Ile Ala Glu Lys
 260 265 270
 Glu Trp Val Tyr Asp Ser His Ser Gln Ala Trp Tyr Tyr Phe Lys Ser
 275 280 285
 Gly Gly Tyr Met Ala Lys Asn Glu Thr Val Asp Gly Tyr Gln Leu Gly
 290 295 300
 Ser Asp Gly Lys Trp Leu Gly Gly Lys Thr Thr Asn Glu Asn Ala Ala
 305 310 315 320
 Tyr Tyr Gln Val Val Pro Val Thr Ala Asn Val Tyr Asp Ser Asp Gly
 325 330 335

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Glu Lys Leu Ser Tyr Ile Ser Gln Gly Ser Val Val Trp Leu Asp Lys
 340 345 350
 Asp Arg Lys Ser Asp Asp Lys Arg Leu Ala Ile Thr Ile Ser Gly Leu
 355 360 365
 Ser Gly Tyr Met Lys Thr Glu Asp Leu Gln Ala Leu Asp Ala Ser Lys
 370 375 380
 Asp Phe Ile Pro Tyr Tyr Glu Ser Asp Gly His Arg Phe Tyr His Tyr
 385 390 395 400
 Val Ala Gln Asn Ala Ser Ile Pro Val Ala Ser His Leu Ser Asp Met
 405 410 415
 Glu Val Gly Lys Lys Tyr Tyr Ser Ala Asp Gly Leu His Phe Asp Gly
 420 425 430
 Phe Lys Leu Glu Asn Pro Phe Leu Phe Lys Asp Leu Thr Glu Ala Thr
 435 440 445
 Asn Tyr Ser Ala Glu Glu Leu Asp Lys Val Phe Ser Leu Leu Asn Ile
 450 455 460
 Asn Asn Ser Leu Leu Glu Asn Lys Gly Ala Thr Phe Lys Glu Ala Glu
 465 470 475 480
 Glu His Tyr His Ile Asn Ala Leu Tyr Leu Leu Ala His Ser Ala Leu
 485 490 495
 Glu Ser Asn Trp Gly Arg Ser Lys Ile Ala Lys Asp Lys Asn Asn Phe
 500 505 510
 Phe Gly Ile Thr Ala Tyr Asp Thr Thr Pro Tyr Leu Ser Ala Lys Thr
 515 520 525
 Phe Asp Asp Val Asp Lys Gly Ile Leu Gly Ala Thr Lys Trp Ile Lys
 530 535 540
 Glu Asn Tyr Ile Asp Arg Gly Arg Thr Phe Leu Gly Asn Lys Ala Ser
 545 550 555 560
 Gly Met Asn Val Glu Tyr Ala Ser Asp Pro Tyr Trp Gly Glu Lys Ile
 565 570 575
 Ala Ser Val Met Met Lys Ile Asn Glu Lys Leu Gly Gly Lys Asp
 580 585 590

(2) INFORMATION FOR SEQ ID NO: 75:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1105 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75: -----

TGGGATTCAA TATGTCAGAG ATGATACTAG AGATAAGAA GAGGGAATAG AGTATGATGA

CGCTGACAAT GGGGATATTA TTGTAAAAGT AGCGACTAAA CCTAAGGTAG TAACCAAGAA 120
 AATTTCAGT ACGCGAATTC GTTATGAAAA AGATGAAACA AAAGACCGTA GTGAAAAATCC 180
 TGTTCACAT GATGGAGAGG ATGGCTATGT AACTACGACA AGGACCTACG ATGTTAATCC 240
 AGAGACTGGT TATGTTACCG AACAGGTTAC TGTGTAGAGA AAAGAAGCCA CGGATACAGT 300
 TATCAAAGTT CCAGCTAAAA GCAAGGTTGA AGAAGTTCTT GTTCCATTG CTACTAAATA 360
 TGAAGCAGAC AATGACCTTT CTGCAGGACA GGAGCAAGAG ATTACTCTAG GAAAGAATGG 420
 GAAAACAGTT ACAACGATAA CTTATAATGT AGATGGAAG AGTGGACAAG TAACTGAGAG 480
 TACTTTAAGT CAAAAAAG ACTCTCAAAC AAGAGTTGTT AAAAAAGaA CCArkCCCCA 540
 AGTCTTGTG CAAGAAATC CAATCGAAAC AGAATATCTC GATGGCCCa CTCTTGATAA 600
 AaGTCAAGAA GTAGAAGAAG TAGGAGAAAT TGGTAAATTA CTCTTACTAC AATCTATACT 660
 GGTAGATGAA CGTGATGGAA CAATTGAAGA AACTACTTCT CGTCAAATTA CTAAGAGAT 720
 GGTAAAAAGA CGTATAAGGA GAGGGACGAG AGAACCTGAA AAGTTGTTG TTCCTGAGCA 780
 ATCATCTATT CCTTCGTATC CTGTATCTGT TACATCTAAC CAAGGAACAG ATGTAGCAGT 840
 AGAACCACT AAAGCAGTTG CTCCAACAAC AGACTGGAAA CAAGAAAATG GTATGTGGTA 900
 TTTTATAAT ACTGATGTT CCATGGCAAC AGGTTGGGTA CAAGTTAATA GTTCATGGTA 960
 CTACCTCAAC AGCAACGTT CTATGAAAGT CAATCAATGG TTCCAAGTTG GTGGTAAATG 1020
 GTATTATGTA AATACATCGG GTGAGTTAGC GGTCAATACA AGTATAGATG GCTATAGAGT 1080
 CAATGATAAT GGTGAATGGG TGCCT 1105

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 368 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Gly Ile Gln Tyr Val Arg Asp Asp Thr Arg Asp Lys Glu Glu Gly Ile
 1 5 10 15
 Glu Tyr Asp Asp Ala Asp Asn Gly Asp Ile Ile Val Lys Val Ala Thr
 20 25 30
 Lys Pro Lys Val Val Thr Lys Lys Ile Ser Ser Thr Arg Ile Arg Tyr
 35 40 45
 Glu Lys Asp Glu Thr Lys Asp Arg Ser Glu Asn Pro Val Thr Ile Asp
 50 55 60
 Gly Glu Asp Gly Tyr Val Thr Thr Thr Arg Thr Tyr Asp Val Asn Pro
 65 70 75 80

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Glu Thr Gly Tyr Val Thr Glu Gln Val Thr Val Asp Arg Lys Glu Ala
 85 90 95
 Thr Asp Thr Val Ile Lys Val Pro Ala Lys Ser Lys Val Glu Glu Val
 100 105 110
 Leu Val Pro Phe Ala Thr Lys Tyr Glu Ala Asp Asn Asp Leu Ser Ala
 115 120 125
 Gly Gln Glu Gln Glu Ile Thr Leu Gly Lys Asn Gly Lys Thr Val Thr
 130 135 140
 Thr Ile Thr Tyr Asn Val Asp Gly Lys Ser Gly Gln Val Thr Glu Ser
 145 150 155 160
 Thr Leu Ser Gln Lys Lys Asp Ser Gln Thr Arg Val Val Lys Lys Arg
 165 170 175
 Thr Xaa Pro Gln Val Leu Val Gln Glu Ile Pro Ile Glu Thr Glu Tyr
 180 185 190
 Leu Asp Gly Pro Thr Leu Asp Lys Ser Gln Glu Val Glu Glu Val Gly
 195 200 205
 Glu Ile Gly Lys Leu Leu Leu Leu Gln Ser Ile Leu Val Asp Glu Arg
 210 215 220
 Asp Gly Thr Ile Glu Glu Thr Thr Ser Arg Gln Ile Thr Lys Glu Met
 225 230 235 240
 Val Lys Arg Arg Ile Arg Arg Gly Thr Arg Glu Pro Glu Lys Val Val
 245 250 255
 Val Pro Glu Gln Ser Ser Ile Pro Ser Tyr Pro Val Ser Val Thr Ser
 260 265 270
 Asn Gln Gly Thr Asp Val Ala Val Glu Pro Ala Lys Ala Val Ala Pro
 275 280 285
 Thr Thr Asp Trp Lys Gln Glu Asn Gly Met Trp Tyr Phe Tyr Asn Thr
 290 295 300
 Asp Gly Ser Met Ala Thr Gly Trp Val Gln Val Asn Ser Ser Trp Tyr
 305 310 315 320
 Tyr Leu Asn Ser Asn Gly Ser Met Lys Val Asn Gln Trp Phe Gln Val
 325 330 335
 Gly Gly Lys Trp Tyr Tyr Val Asn Thr Ser Gly Glu Leu Ala Val Asn
 340 345 350
 Thr Ser Ile Asp Gly Tyr Arg Val Asn Asp Asn Gly Glu Trp Val Arg
 355 360 365

(2) INFORMATION FOR SEQ ID NO: 77:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 661 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

00755272.012201

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

GGATAATAGA GAAGCATTAA AAACCTTTAT GACGGGTGAA AATTTTATC TCCAACATTA 50
 TCTAGGAGCA CATAGGGAAG AACTAAATGG AGAGCATGGC TATACCTTCC GTGTTTGGGC 120
 ACCTAATGCT CAGGCTGTTC ACTTGTTGG TGATTTTACC AACTGGATTG AAAATCAGAT 180
 TCCAATGGTA AGAAATGATT TTGGGGTCTG GGAAGTCTTT ACCAATATGG CTCAGAAGG 240
 GCATATTTAC AAATATCATG TCACACGTCA AAATGGTCAT CAACTGATGA AGATTGACCC 300
 TTTTGCTGTC AGGTATGAGS CTCGTCCAGG AACAGGGGCA ATCGTAACAG AGCTTCCTGA 360
 GAAGAAATGG AAGGATGGAC TTTGGCTGGC ACGAAGAAAA CGTTGGGGCT TTGAAGAGCG 420
 TCCTGTCAAT ATTTATGAAG TTCACGCTGG ATCATGGAAA AGAAATTCTG ATGGCAGTCC 480
 TTATAGTTT GCCCAGCTCA AGGATGAAC TATTCCTTAT CTCGTTGAAA TGAATATAC 540
 TCATATTGAG TTTATGCCCT TGATGTCCCA TCCTTTGGGC TTGAGTTGGG GGTATCAGCT 600
 TATGGGTTAC TTCGCTTAC AGCATGCTTA TGGCCGACCA GAGGAGTTTC AAGATTTTGT 660
 C 661

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 220 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Asp Asn Arg Glu Ala Leu Lys Thr Phe Met Thr Gly Glu Asn Phe Tyr
 1 5 10 15
 Leu Gln His Tyr Leu Gly Ala His Arg Glu Glu Leu Asn Gly Glu His
 20 25 30
 Gly Tyr Thr Phe Arg Val Trp Ala Pro Asn Ala Gln Ala Val His Leu
 35 40 45
 Val Gly Asp Phe Thr Asn Trp Ile Glu Asn Gln Ile Pro Met Val Arg
 50 55 60
 Asn Asp Phe Gly Val Trp Glu Val Phe Thr Asn Met Ala Gln Glu Gly
 65 70 75 80
 His Ile Tyr Lys Tyr His Val Thr Arg Gln Asn Gly His Gln Leu Met
 85 90 95
 Lys Ile Asp Pro Phe Ala Val Arg Tyr Glu Ala Arg Pro Gly Thr Gly
 100 105 110
 Ala Ile Val Thr Glu Leu Pro Glu Lys Lys Trp Lys Asp Gly Leu Trp

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 102210-22560

115	120	125
Leu Ala Arg Arg Lys Arg Trp Gly Phe Glu Glu Arg Pro Val Asn Ile		
130	135	140
Tyr Glu Val His Ala Gly Ser Trp Lys Arg Asn Ser Asp Gly Ser Pro		
145	150	155
Tyr Ser Phe Ala Gln Leu Lys Asp Glu Leu Ile Pro Tyr Leu Val Glu		
165	170	175
Met Asn Tyr Thr His Ile Glu Phe Met Pro Leu Met Ser His Pro Leu		
180	185	190
Gly Leu Ser Trp Gly Tyr Gln Leu Met Gly Tyr Phe Ala Leu Glu His		
195	200	205
Ala Tyr Gly Arg Pro Glu Glu Phe Gln Asp Phe Val		
210	215	220

(2) INFORMATION FOR SEQ ID NO: 79:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 976 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

AGATTTTGTC GAGGAGTGTC ATACCCATAA TATTGGGGTT ATGTGGGACT GGGTACCAGN	60
TCACCTTACC ATCAACGATG ATGCCTTAGC CTATTATGAT GGGACACCGA CTTTGAATA	120
CCAAGACCAT AATAAGGCTC ATAACCATGG TTGGGGTGCC CTTAATTTTG ACCTTGGA	180
AAATGAAGTC CAGTCCTTCT TAATTCTTG CATTAAGCAT TGGATTGATG TCTATCATT	240
GGATGGTATT CGTGTGGATG CTGTTAGCAA CATGCTCTAT TTGGACTATG ATGATGCTCC	300
ATGGACACCT AATAAAGATG GCGGAAATCT CAACTATGAA GGTATTATT TCTTCACGC	360
CTTGAATGAG GTTATTAAGT TAGAATATCC AGATGTGATG ATGATTGCAG AAGAAAGTTC	420
GTCTGCGATC AAGATTACGG GAATGAAAGA GATTGGTGGT CTAGGATTG ACTACAATG	480
GAACATGGGC TGGATGAATG ATATCCTCCG TTTCTACGAA GAAGATCCGA TCTATCGTAA	540
ATATGACTTT AACCTGGTGA CTTTCAGCTT TATGTATGTT TNCAAGSAGA ATTATCTCTT	600
GCCATTCTCG CACGATGAAG TGGTTCATGG CAAGAAGATG ATGATGCATA AGATGTGGGG	660
AGATCGTTAC AATCAATTGC CAGGCTTGCG CAATCTCTAT ACGTACCAAA TTTGTCACCC	720
TGGTAAGAAA TTGCTCTTCA TGGGTAGCGA ATACGGTCAA TTCCTAGAAT GGAATCTGTA	780
AGAACAGTTG GAATGGTCTA ACCTAGAAGA CCAATGAAT GCTAAGATGA AGTATTTCGC	840
TTCTCAGCTA AACCAGTTTT ACAAGATCA TCGCTGCTG TGGGAAATTG ATACCAGCTA	900
TGATGGTATT GAAATCATTG ATCGGATAA TCGAGACCAG AGTGTTCTTT CCTTTATTGC	960

TAAGGGTAAA AAGGGA

976

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

```

Asp Phe Val Glu Glu Cys His Thr His Asn Ile Gly Val Ile Val Asp
 1             5             10             15

Trp Val Pro Xaa His Phe Thr Ile Asn Asp Asp Ala Leu Ala Tyr Tyr
      20             25             30

Asp Gly Thr Pro Thr Phe Glu Tyr Gln Asp His Asn Lys Ala His Asn
      35             40             45

His Gly Trp Gly Ala Leu Asn Phe Asp Leu Gly Lys Asn Glu Val Gln
      50             55             60

Ser Phe Leu Ile Ser Cys Ile Lys His Trp Ile Asp Val Tyr His Leu
 65             70             75             80

Asp Gly Ile Arg Val Asp Ala Val Ser Asn Met Leu Tyr Leu Asp Tyr
      85             90             95

Asp Asp Ala Pro Trp Thr Pro Asn Lys Asp Gly Gly Asn Leu Asn Tyr
      100            105            110

Glu Gly Tyr Tyr Phe Leu Gln Arg Leu Asn Glu Val Ile Lys Leu Glu
      115            120            125

Tyr Pro Asp Val Met Met Ile Ala Glu Glu Ser Ser Ser Ala Ile Lys
      130            135            140

Ile Thr Gly Met Lys Glu Ile Gly Gly Leu Gly Phe Asp Tyr Lys Trp
      145            150            155            160

Asn Met Gly Trp Met Asn Asp Ile Leu Arg Phe Tyr Glu Glu Asp Pro
      165            170            175            180

Ile Tyr Arg Lys Tyr Asp Phe Asn Leu Val Thr Phe Ser Phe Met Tyr
      180            185            190

Val Xaa Lys Glu Asn Tyr Leu Leu Pro Phe Ser His Asp Glu Val Val
      195            200            205

His Gly Lys Lys Ser Met Met His Lys Met Trp Gly Asp Arg Tyr Asn
      210            215            220

Gln Phe Ala Gly Leu Arg Asn Leu Tyr Thr Tyr Gln Ile Cys His Pro
      225            230            235            240

Gly Lys Lys Leu Leu Phe Met Gly Ser Glu Tyr Gly Gln Phe Leu Glu
      245            250            255

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Trp Lys Ser Glu Glu Gln Leu Glu Trp Ser Asn Leu Glu Asp Pro Met
 260 265 270

Asn Ala Lys Met Lys Tyr Phe Ala Ser Gln Leu Asn Gln Phe Tyr Lys
 275 280 285

Asp His Arg Cys Leu Trp Glu Ile Asp Thr Ser Tyr Asp Gly Ile Glu
 290 295 300

Ile Ile Asp Ala Asp Asn Arg Asp Gln Ser Val Leu Ser Phe Ile Arg
 305 310 315 320

Lys Gly Lys Lys Gly
 325

(2) INFORMATION FOR SEQ ID NO: 81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2134 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

ATCTGTAGTT TATGCGGATG AAACACTTAT TACTCATACT GCTGAGAAAC CTAAGAGGGA 60

AAAAATGATA GTAGAAGAAA AGGCTGATAA AGCTTTGGAA ACTAAAAATA TAGTTGAAAG 120

GACAGAACAA AGTGAACTTA GTTCAACTGA GGCATTGCA TCTGAGNAGA AAGAAGATGA 180

AGCCGTAACCT CCAAAAGAGG AAAAAGTGTC TGCTAAACCG GAAGAAAAG CTCCAAGGAT 240

AGAATCACAA GCTTCAAAATC AAGAAAAACC GCTCAAGGAA GATGCTAAAG CTGTAAACAA 300

TGAAGAAGTG AATCAAAATGA TTGAAGACAG GAAAGTGGAT TTTAATCAAA ATTGGTACTT 360

TAAACTCAAT GCAAAATTCTA AGGAAGCCAT TAAACCTGAT GCAGACGTAT CTACGTGGAA 420

AAAATTAGAT TTACCGTATG ACTGGAGTAT CTTTAAACGAT TTCGATCATG AATCTCCTGC 480

ACAAAATGAA GGTGGACAGC TCAACGGTGG GGAAGCTTGG TATCGCAAGA CTTTCAAACT 540

AGATGAAAAA GACCTCAAGA AAAATGTTTCG CTTACTTTT GATGGCGTCT ACATGGATTTC 600

TCAAGTTTAT GTCAATGGTC AGTTAGTGGG GCATTATCCA AATGGTTATA ACCAGTTCTC 660

ATATGATATC ACCAAATACC TTCAAAAAGA TGGTCGTGAG AATGTGATTG CTGTCCATGC 720

AGTCAACAAA CAGCCAAGTA GCGTGTGGTA TTCAGGAAGT GGTATCTATC GTGATGTGAC 780

TTTACAAGTG ACAGATAAGG TGCATGTTGA GAAAAATGGG ACAACTATTT TAACACCAAA 840

ACTTGAAGAA CAACAACATG GCAAGGTTGA AACTCATGTG ACCAGCAAAA TCGTCAATAC 900

GGACGACAAA GACCATGAAC TTGTAGCCGA ATATCAAATC GTTGAACGAG GTGGTCATGC 960

TGTAACAGGC TTAGTTCGTA CAGCGAGTCG TACCTTAAAA GCACATGAAT CAACAAGCCT 1020

AGATGCGATT TTGAAGTTG AAAGACCAAA ACTCTGGACT GTTTTAAATG ACAAACTGCG 1080

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CTTGTACGAA TTGATTACGC GTGTTTACCG TGACGGTCAA TTGGTTGATG CTAAGAAGGA 1140
 TTTGTTTGGT TACCGTTACT ATCACTGGAC TCCAATGAA GGTTCCTCTT TGAATGGTGA 1200
 ACGTATTAATA TTCCATGGAG TATCCTTGCA CCACGACCAT GGGGCGCTTG GAGCAGAAGA 1260
 AAACATAAAA GCAGAATATC GCCGTCTCAA ACAATGAAG GAGATGGGAG TTAATCCAT 1320
 CCGTACAACC CACAACCCCTG CTAGTGAGCA AACCTTGCAA ATCGCAGCAG AACTAGGTTT 1380
 ACTCGTTACG GAAGAGGCCT TTGATACGTG GTATGGTGGC AAGAAACCTT ATGACTATGG 1440
 ACGTTTCTTT GAAAAGATG CCACTCACCC AGAAGCTCGA AAAGGTGAAA AATGGTCTGA 1500
 TTTTGACCTA CGTACCATGG TCGAAAGAGG CAAAAACAAC CCTGCTATCT TCATGTGGTC 1560
 AATTGGTAAT GAAATAGGTG AAGCTAATGG TGATGCCAC TCTTTAGCAA CTGTTAAACG 1620
 TTTGGTTAAG GTTATCAAGG ATGTTGATAA GACTCGCTAT GTTACCATGG GAGCAGATAA 1680
 ATTCGGTTTC GGTAATGGTA GCGGAGGGCA TGAGAAAATT GCTGATGAAC TCGATGCTGT 1740
 TGGATTTAAC TATTCTGAAG ATAATTACAA AGCCCTTAGA GCTAAGCATC CAAAATGGTT 1800
 GATTTATGGA TCAGAAACAT CTTCACTAC CCGTACAGT GGAAGTTACT ATCGCCCTGA 1860
 ACGTGAATYG AAACATAGCA ATGGACCTGA GCGTAATTAT GAACAGTCAG ATTATGGAAA 1920
 TGATCGTGTG GGTGGGGGA AAACAGCAAC CGCTTCATGG ACTTTTGACC GTGACAACGC 1980
 TGGCTATGCT GGACAGTTTA TCTGGACAGS TACGGACTAT ATTGGTGAAC CTACACCATG 2040
 GCACAACCAA AATCAAACCT CTGTTAAGAG CTCTTACTTT GGTATCGTAG ATACAGCCGG 2100
 CATTCCAAAA CATGACTTCT ATCTCTACCA AAGC 2134

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 711 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Ser Val Val Tyr Ala Asp Glu Thr Leu Ile Thr His Thr Ala Glu Lys
 1 5 10 15

Pro Lys Glu Glu Lys Met Ile Val Glu Glu Lys Ala Asp Lys Ala Leu
 20 25 30

Glu Thr Lys Asn Ile Val Glu Arg Thr Glu Gln Ser Glu Pro Ser Ser
 35 40 45

Thr Glu Ala Ile-Ala Ser Glu Xaa Lys Glu Asp Glu Ala Val Thr Pro
 50 55 60

Lys Glu Glu Lys Val Ser Ala Lys Pro Glu Glu Lys Ala Pro Arg Ile

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65		70		75		80
Glu Ser Gln Ala Ser Asn Gln Glu Lys Pro Leu Lys Glu Asp Ala Lys						
		85		90		95
Ala Val Thr Asn Glu Glu Val Asn Gln Met Ile Glu Asp Arg Lys Val						
	100			105		110
Asp Phe Asn Gln Asn Trp Tyr Phe Lys Leu Asn Ala Asn Ser Lys Glu						
	115			120		125
Ala Ile Lys Pro Asp Ala Asp Val Ser Thr Trp Lys Lys Leu Asp Leu						
	130		135		140	
Pro Tyr Asp Trp Ser Ile Phe Asn Asp Phe Asp His Glu Ser Pro Ala						
	145		150		155	160
Gln Asn Glu Gly Gly Gln Leu Asn Gly Gly Glu Ala Trp Tyr Arg Lys						
		165		170		175
Thr Phe Lys Leu Asp Glu Lys Asp Leu Lys Lys Asn Val Arg Leu Thr						
	180			185		190
Phe Asp Gly Val Tyr Met Asp Ser Gln Val Tyr Val Asn Gly Gln Leu						
	195		200		205	
Val Gly His Tyr Pro Asn Gly Tyr Asn Gln Phe Ser Tyr Asp Ile Thr						
	210		215		220	
Lys Tyr Leu Gln Lys Asp Gly Arg Glu Asn Val Ile Ala Val His Ala						
	225		230		235	240
Val Asn Lys Gln Pro Ser Ser Arg Trp Tyr Ser Gly Ser Gly Ile Tyr						
		245		250		255
Arg Asp Val Thr Leu Gln Val Thr Asp Lys Val His Val Glu Lys Asn						
	260			265		270
Gly Thr Thr Ile Leu Thr Pro Lys Leu Glu Glu Gln Gln His Gly Lys						
	275			280		285
Val Glu Thr His Val Thr Ser Lys Ile Val Asn Thr Asp Asp Lys Asp						
	290		295		300	
His Glu Leu Val Ala Glu Tyr Gln Ile Val Glu Arg Gly Gly His Ala						
	305		310		315	320
Val Thr Gly Leu Val Arg Thr Ala Ser Arg Thr Leu Lys Ala His Glu						
		325		330		335
Ser Thr Ser Leu Asp Ala Ile Leu Glu Val Glu Arg Pro Lys Leu Trp						
	340			345		350
Thr Val Leu Asn Asp Lys Pro Ala Leu Tyr Glu Leu Ile Thr Arg Val						
	355			360		365
Tyr Arg Asp Gly Gln Leu Val Asp Ala Lys Lys Asp Leu Phe Gly Tyr						
	370		375		380	
Arg Tyr Tyr His Trp Thr Pro Asn Glu Gly Phe Ser Leu Asn Gly Glu						
	385		390		395	400
Arg Ile Lys Phe His Gly Val Ser Leu His His Asp His Gly Ala Leu						

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405 410 415
 Gly Ala Glu Glu Asn Tyr Lys Ala Glu Tyr Arg Arg Leu Lys Gln Met
 420 425 430
 Lys Glu Met Gly Val Asn Ser Ile Arg Thr Thr His Asn Pro Ala Ser
 435 440 445
 Glu Gln Thr Leu Gln Ile Ala Ala Glu Leu Gly Leu Leu Val Gln Glu
 450 455 460
 Glu Ala Phe Asp Thr Trp Tyr Gly Gly Lys Lys Pro Tyr Asp Tyr Gly
 465 470 475 480
 Arg Phe Phe Glu Lys Asp Ala Thr His Pro Glu Ala Arg Lys Gly Glu
 485 490 495
 Lys Trp Ser Asp Phe Asp Leu Arg Thr Met Val Glu Arg Gly Lys Asn
 500 505 510
 Asn Pro Ala Ile Phe Met Trp Ser Ile Gly Asn Glu Ile Gly Glu Ala
 515 520 525
 Asn Gly Asp Ala His Ser Leu Ala Thr Val Lys Arg Leu Val Lys Val
 530 535 540
 Ile Lys Asp Val Asp Lys Thr Arg Tyr Val Thr Met Gly Ala Asp Lys
 545 550 555 560
 Phe Arg Phe Gly Asn Gly Ser Gly Gly His Glu Lys Ile Ala Asp Glu
 565 570 575
 Leu Asp Ala Val Gly Phe Asn Tyr Ser Glu Asp Asn Tyr Lys Ala Leu
 580 585 590
 Arg Ala Lys His Pro Lys Trp Leu Ile Tyr Gly Ser Glu Thr Ser Ser
 595 600 605
 Ala Thr Arg Thr Arg Gly Ser Tyr Tyr Arg Pro Glu Arg Glu Leu Lys
 610 615 620
 His Ser Asn Gly Pro Glu Arg Asn Tyr Glu Gln Ser Asp Tyr Gly Asn
 625 630 635 640
 Asp Arg Val Gly Trp Gly Lys Thr Ala Thr Ala Ser Trp Thr Phe Asp
 645 650 655
 Arg Asp Asn Ala Gly Tyr Ala Gly Gln Phe Ile Trp Thr Gly Thr Asp
 660 665 670
 Tyr Ile Gly Glu Pro Thr Pro Trp His Asn Gln Asn Gln Thr Pro Val
 675 680 685
 Lys Ser Ser Tyr Phe Gly Ile Val Asp Thr Ala Gly Ile Pro Lys His
 690 695 700
 Asp Phe Tyr Leu Tyr Gln Ser
 705 710

(2) INFORMATION FOR SEQ ID NO: 83:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2167 base pairs

0075272.012201

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

TTACTTTGGT ATCGTAGATA CAGCCGGCAT TCCTAAACAT GACTTCTATC TCTACCAAG	60
CCAATGGGTT TCTGTTAAGA AGAAACCGAT GGTACACCTT CTTCTCTACT GGAACGGGA	120
AAACAAAGAA TTAGCATCCA AAGTAGCTGA CTCAGAAGGT AAGATTCCAG TTCGTGCTTA	180
TTCGAATGCT TCTAGTGTAG AATTGTTCTT GAATGGAAAA TCTCTGGTC TTAAGACTTT	240
CAATAAAAAA CAAACCAGCG ATGGCGGGAC TTACCAAGAA GGTGCAAATG CTAATGAACT	300
TTATCTTGAA TGGAAAGTTG CCTATCAACC AGGTACCTTG GAAGCAATTG CTCGTGATGA	360
ATCTGGCAAG GAAATGCTC GAGATAAGAT TACGACTGCT GGTAGCCAG CGGCAGTTTCG	420
TCTTATTAAG GAAGACCATG CGATTGCAGC AGATGGAAAA GACTTGACTT ACATCTACTA	480
TGAAATGTGT GACAGCCAGG GGAATGTGGT TCCAACGTCT AATAATCTGG TTCGCTTCCA	540
ATTGCATGGC CAAGGTCAAC TGGTCGGTGT AGATAACGGA GAACAAGCCA GCCGTGAACG	600
CTATAAGCGG CAAGCAGATG GTTCTTGGAT TCGTAAAGCA TTTAATGGTA AAGGTGTTGC	660
CATTGTCAAA TCAACTGAAC AAGCAGGGAA ATTACCCCTG ACTGCCACT CTGATCTCTT	720
GAAATCGAAC CAAGTCACTG TCTTTACTGG TAAGAAAGAA GGACAAGAGA AGACTGTTTT	780
GGGGACAGAA GTGCCAAAAG TACAGACCAT TATTGGAGAG GCACCTGAAA TGCCCTACCAC	840
TGTTCCGTTT GTATACAGTG ATGGTAGCCG TGCAGAACGT CCTGTAACCT GGTCTTCAGT	900
AGATGTGAGC AAGCCTGGTA TTGTAACGGT GAAAGGTATG GCTGACGGAC GAGAAGTAGA	960
AGCTCGTGTA GAAGTGATTG CTCTTAAATC AGAGCTACCA GTTGTGAAAC GTATTGCTCC	1020
AAATACTGAC TTGAATCTCT TAGACAAATC TGTTCCTAT GTTTTGATTG ATGGAAGTGT	1080
TGAAGAGTAT GAAGTGGACA AGTGGGAGAT TGCCGAAGAA GATAAAGCTA AGTTAGCAAT	1140
TCCAGGTTCT CGTATTCAAG CGACCGGTTA TTTAGAAGGT CAACCAATTC ATGCAACCTT	1200
TGTGTTAGAA GAAGGCAATC CTGCGGCACC TGCAGTACCA ACTGTAAACG TGTGTTGTTGA	1260
GGCAGTAACA GGTCTTACTA GTCAAAAACC AATGCAATAC CGCACTCTTG CTTATTGGAGC	1320
TAAGTTGCCA GAAGTCACAG CAAGTGCTAA AAATGCAGCT GTTACAGTTC TTCAAGCAAG	1380
CGCAGCAAAC GGCATGCGTG CGAGCATCTT TATTCAGCCT AAAGATGGTG GCCTCTTCTA	1440
AACCTATGCA ATTCAATTC TTGAAGAAGC GCCAAAATTT GCTCACTTGA GCTTGCAAGT	1500
GGAAAAGCT GACAGTCTCA AAGAAGACCA AACTGTCAAA TTGTCGGTTC GAGTCACTA	1560
TCAAGATGGA ACGCAAGCTG TATTACCAGC TGATAAAGTA ACCTTCTCTA CAAGTGGTGA	1620
AGGGGAAGTC GCAATTCGTA AAGGAATGCT TGAGTTGCAT AAGCCAGGAG CAGTCACTCT	1680

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GAACGCTGAA TATGAGGGAG CTAAAGACCA AGTTGAACTC ACTATCCAAG CCAACTACTGA 1740
 GAAGAAGATT GCGCAATCCA TCCGTCCTGT AAATGTAGTG ACAGATTTCG ATCAGGAACC 1800
 AAGTCTTCCA GCAACAGTAA CAGTTGAGTA TGACAAAGGT TTCCCTAAAA CTCATAAAGT 1860
 CACTTGGCAA GCTATTCCGA AAGAAAAACT AGACTCCTAT CAAACATTTC AAGTACTAGG 1920
 TAAAGTTGAA GGAATTGACC TTGAAGCGCG TGCAAAAGTC TCTGTAGAAG GTATCGTTTC 1980
 AGTTGAAGAA GTCAGTGTGA CAACTCCAAT CGCAGAAGCA CCACAATTAC CAGAAAGTGT 2040
 TCGGACATAT GATTCAAATG GTCACGTTC ATCAGCTAAG GTTGCATGGG ATGCGATTTC 2100
 TCCAGAGCAA TACGCTAAGG AAGGTGTCTT TACAGTTAAT GGTGCTTAG AAGGTACGCA 2160
 ATTAACA 2167

(2) INFORMATION FOR SEQ ID NO:84:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 722 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

Tyr Phe Gly Ile Val Asp Thr Ala Gly Ile Pro Lys His Asp Phe Tyr
 1 5 10 15
 Leu Tyr Gln Ser Gln Trp Val Ser Val Lys Lys Lys Pro Met Val His
 20 25 30
 Leu Leu Pro His Trp Asn Trp Glu Asn Lys Glu Leu Ala Ser Lys Val
 35 40 45
 Ala Asp Ser Glu Gly Lys Ile Pro Val Arg Ala Tyr Ser Asn Ala Ser
 50 55 60
 Ser Val Glu Leu Phe Leu Asn Gly Lys Ser Leu Gly Leu Lys Thr Phe
 65 70 75 80
 Asn Lys Lys Gln Thr Ser Asp Gly Arg Thr Tyr Gln Glu Gly Ala Asn
 85 90 95
 Ala Asn Glu Leu Tyr Leu Glu Trp Lys Val Ala Tyr Gln Pro Gly Thr
 100 105 110
 Leu Glu Ala Ile Ala Arg Asp Glu Ser Gly Lys Glu Ile Ala Arg Asp
 115 120 125
 Lys Ile Thr Thr Ala Gly Lys Pro Ala Ala Val Arg Leu Ile Lys Glu
 130 135 140
 Asp His Ala Ile Ala Ala Asp Gly Lys Asp Leu Thr Tyr Ile Tyr Tyr
 145 150 155 160
 Glu Ile Val Asp Ser Gln Gly Asn Val Val Pro Thr Ala Asn Asn Leu

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165

170

175

Val Arg Phe Gln Leu His Gly Gln Gly Gln Leu Val Gly Val Asp Asn
 180 185 190

Gly Glu Gln Ala Ser Arg Glu Arg Tyr Lys Ala Gln Ala Asp Gly Ser
 195 200 205

Trp Ile Arg Lys Ala Phe Asn Gly Lys Gly Val Ala Ile Val Lys Ser
 210 215 220

Thr Glu Gln Ala Gly Lys Phe Thr Leu Thr Ala His Ser Asp Leu Leu
 225 230 235 240

Lys Ser Asn Gln Val Thr Val Phe Thr Gly Lys Lys Glu Gly Gln Glu
 245 250 255

Lys Thr Val Leu Gly Thr Glu Val Pro Lys Val Gln Thr Ile Ile Gly
 260 265 270

Glu Ala Pro Glu Met Pro Thr Thr Val Pro Phe Val Tyr Ser Asp Gly
 275 280 285

Ser Arg Ala Glu Arg Pro Val Thr Trp Ser Ser Val Asp Val Ser Lys
 290 295 300

Pro Gly Ile Val Thr Val Lys Gly Met Ala Asp Gly Arg Glu Val Glu
 305 310 315 320

Ala Arg Val Glu Val Ile Ala Leu Lys Ser Glu Leu Pro Val Val Lys
 325 330 335

Arg Ile Ala Pro Asn Thr Asp Leu Asn Ser Val Asp Lys Ser Val Ser
 340 345 350

Tyr Val Leu Ile Asp Gly Ser Val Glu Glu Tyr Glu Val Asp Lys Trp
 355 360 365

Glu Ile Ala Glu Glu Asp Lys Ala Lys Leu Ala Ile Pro Gly Ser Arg
 370 375 380

Ile Gln Ala Thr Gly Tyr Leu Glu Gly Gln Pro Ile His Ala Thr Leu
 385 390 395 400

Val Val Glu Glu Gly Asn Pro Ala Ala Pro Ala Val Pro Thr Val Thr
 405 410 415

Val Gly Gly Glu Ala Val Thr Gly Leu Thr Ser Gln Lys Pro Met Gln
 420 425 430

Tyr Arg Thr Leu Ala Tyr Gly Ala Lys Leu Pro Glu Val Thr Ala Ser
 435 440 445

Ala Lys Asn Ala Ala Val Thr Val Leu Gln Ala Ser Ala Ala Asn Gly
 450 455 460

Met Arg Ala Ser Ile Phe Ile Gln Pro Lys Asp Gly Gly Pro Leu Gln
 465 470 475 480

Thr Tyr Ala Ile Gln Phe Leu Glu Glu Ala Pro Lys Ile Ala His Leu
 485 490 495

Ser Leu Gln Val Glu Lys Ala Asp Ser Leu Lys Glu Asp Gln Thr Val

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202

500	505	510
Lys Leu Ser Val Arg Ala His Tyr Gln Asp Gly Thr Gln Ala Val Leu		
515	520	525
Pro Ala Asp Lys Val Thr Phe Ser Thr Ser Gly Glu Gly Glu Val Ala		
530	535	540
Ile Arg Lys Gly Met Leu Glu Leu His Lys Pro Gly Ala Val Thr Leu		
545	550	555
Asn Ala Glu Tyr Glu Gly Ala Lys Asp Gln Val Glu Leu Thr Ile Gln		
565	570	575
Ala Asn Thr Glu Lys Lys Ile Ala Gln Ser Ile Arg Pro Val Asn Val		
580	585	590
Val Thr Asp Leu His Gln Glu Pro Ser Leu Pro Ala Thr Val Thr Val		
595	600	605
Glu Tyr Asp Lys Gly Phe Pro Lys Thr His Lys Val Thr Trp Gln Ala		
610	615	620
Ile Pro Lys Glu Lys Leu Asp Ser Tyr Gln Thr Phe Glu Val Leu Gly		
625	630	635
Lys Val Glu Gly Ile Asp Leu Glu Ala Arg Ala Lys Val Ser Val Glu		
645	650	655
Gly Ile Val Ser Val Glu Glu Val Ser Val Thr Thr Pro Ile Ala Glu		
660	665	670
Ala Pro Gln Leu Pro Glu Ser Val Arg Thr Tyr Asp Ser Asn Gly His		
675	680	685
Val Ser Ser Ala Lys Val Ala Trp Asp Ala Ile Arg Pro Glu Gln Tyr		
690	695	700
Ala Lys Glu Gly Val Phe Thr Val Asn Gly Arg Leu Glu Gly Thr Gln		
705	710	715
		720
Leu Thr		

(2) INFORMATION FOR SEQ ID NO: 85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2329 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

AGCTAAGGTT GCATGGGATG CGATTTCGTCC AGAGCAATAC GCTAAGGAAG GTGTCTTTAC	60
AGTTAATGGT CGCTTAGAAG GTACGCAATT AACAACTAAA CTTTCATGTTT CGGTATCTGC	120
TCAAACCTGAG CAAGGTGCAA ACATTTCTGA CCAATGGACC GGTTCAGAAT TGCCACTTGC	180
CTTTGCTTCA GACTCAAATC CAAGCGACCC AGTTTCAAAT GTTAATGACA AGCTCATTTT	240

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CTACAATAAC CAACCAGCCA ATCGTTGGAC AAACCTGGAAT CGTACTAATC CAGAAGCTTC	300
AGTCGGTGGT CTGTTTGGAG ATTCAGGTAT CTTGAGCAAA CGCTCCGTTG ATAATCTAAG	360
TGTCGGATTC CATGAAGACC ATGGAGTTGG TGTACCGAAG TCTTATGTGA TTGAGTATTA	420
TGTTGGTAAG ACTGTCCCAA CAGCTCCTAA AAACCCTAGT TTTGTTGSTA ATGAGGACCA	480
TGTCCTTAAT GATTCTGCCA ACTGGAAACC AGTTACTAAT CTAAAAGCCC CTGCTCAACT	540
CAAGGCTGGA GAAATGAACC ACTTTAGCTT TGATAAAGTT GAAACCTATG CTGTTCTGAT	600
TCGCATGGTT AAAGCAGATA ACAAGCGTGG AACGCTCTATC ACAGAGGTAC AAATCTTTGC	660
GAAACAAGTT GCGGCAGCCA AGCAAGGACA AACAGAATC CAAGTTGACG GCAAAGACTT	720
AGCAAATTC AACCTGATT TGACAGACTA CTACCTTGAG TCTGTAGATG GAAAAGTTCC	780
GGCAGTCACA GCAAGTGTTA GCAACAATGG TCTCGCTACC GTCGTTCCAA GCGTTCGTGA	840
AGGTGAGCCA GTTCGTGTCA TCGCGAAAGC TGAATAAGGC GACATCTTAG GAGAATACCG	900
TCTGCACTTC ACTAAGGATA AGAGCTTACT TTCTCATAAA CCAGTTGCTG CGGTAAACA	960
AGCTCGCTTG CTACAAGTAG GTCAAGCACT TGAATTGCCG ACTAAGGTTT CAGTTTACTT	1020
CACAGGTAAA GACGGCTACG AAACAAAAGA CCTGACAGTT GAATGGGAAG AAGTTCACGC	1080
GGAAAATCTG ACAAAGCAG GTCAATTAC TGTTCGAGGC CGTGTCTCTG GTAGTAACCT	1140
TGTTGCTGAG ATCACTGTAC GAGTGACAGA CAAACTTGGT GAGACTCTTT CAGATAACCC	1200
TAATATGAT GAAAACAGTA ACCAGGCCCT TGCTTCAGCA ACCAATGATA TTGACAAAAA	1260
CTCTCATGAC CGCGTTGACT ATCTCAATGA CGGAGATCAT TCAGAAAATC GTCGTTGGAC	1320
AAACTGGTCA CCAACACCAT CTCTAATCC AGAAGTATCA GCGGGTGTGA TTTTCCGTGA	1380
AAATGGTAAG ATTGTAGAAC GGAAGTTTAC ACAAGGAAAA GTTCAGTTCT TTGCAGATAG	1440
TGTCACGGAT GCACCATCTA AACTCGTTTT AGAAGCGTAT GTGCGTCCAG AGTTTGAAGT	1500
GCCAACCTAC TATTCAAACT ACCAAGCCTA CGACGCAGAC CATCCATTCA ACAATCCAGA	1560
AAATTGGGAA GCTGTTCCCT ATCGTGCAGA TAAAGACATT GCAGCTGGTG ATGAAATCAA	1620
CGTAACATTT AAAGCTATCA AAGCCAAAGC TATGAGATGG CGTATGGAGC GTAAAGCAGA	1680
TAAGAGCGGT GTTGCAGTGA TTGAGATGAC CTTCTTGCA CCAAGTGAAT TGCTCAAGA	1740
AAGCACTCAA TCAAAGATT TGTAGATGG AAAAGAACTT GCTGATTTCC CTGAAAATCG	1800
TCAAGACTAT CAAATTACCT ATAAAGGTCA ACGGCCAAAA GTCTCAGTTG AAGAAAACAA	1860
TCAAGTAGCT TCAACTGTGG TAGATAGTGG AGAAGATAGC TTTCAGTAC TTGTTGCGCT	1920
CGTTTCAGAA AGTGAAAAAC AAGTCAAGGA ATACCGTATC CACTTGACTA AGGAAAAACC	1980
AGTTTCTGAG AAGACAGTTG CTGCTGTACA AGAAGATCTT CCAAAAATCG AATTTGTTGA	2040
AAAAGATTTG GCATACAAGA CAGTTGAGAA AAAAGATTCA AACTGTATC TAGGTGAAC	2100

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TCGTGTAGAA CAAGAAGGAA AAGTTGGAAG AGAAGGTATC TTACAGCGA TTAATCCTGA 2160
 TGGAAGTAAG GAAGAAAAAC TCCGTGAAGT GGTAGAAGTT CCGACAGACC GCATCGTCTT 2220
 GGTGGAAC AAACAGTAG CTCAGAAGC TAAAAACCA CAAGTGTGAG AAAAGCAGA 2280
 TACAAAAACCA ATTGATTCAA GTGAAGCTAG TCAAATAAT AAAGCCCAG 2329

(2) INFORMATION FOR SEQ ID NO:86:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 776 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

Ala Lys Val Ala Trp Asp Ala Ile Arg Pro Glu Gln Tyr Ala Lys Glu
 1 5 10 15
 Gly Val Phe Thr Val Asn Gly Arg Leu Glu Gly Thr Gln Leu Thr Thr
 20 25 30
 Lys Leu His Val Arg Val Ser Ala Gln Thr Glu Gln Gly Ala Asn Ile
 35 40 45
 Ser Asp Gln Trp Thr Gly Ser Glu Leu Pro Leu Ala Phe Ala Ser Asp
 50 55 60
 Ser Asn Pro Ser Asp Pro Val Ser Asn Val Asn Asp Lys Leu Ile Ser
 65 70 75 80
 Tyr Asn Asn Gln Pro Ala Asn Arg Trp Thr Asn Trp Asn Arg Thr Asn
 85 90 95
 Pro Glu Ala Ser Val Gly Val Leu Phe Gly Asp Ser Gly Ile Leu Ser
 100 105 110
 Lys Arg Ser Val Asp Asn Leu Ser Val Gly Phe His Glu Asp His Gly
 115 120 125
 Val Gly Val Pro Lys Ser Tyr Val Ile Glu Tyr Tyr Val Gly Lys Thr
 130 135 140
 Val Pro Thr Ala Pro Lys Asn Pro Ser Phe Val Gly Asn Glu Asp His
 145 150 155 160
 Val Phe Asn Asp Ser Ala Asn Trp Lys Pro Val Thr Asn Leu Lys Ala
 165 170 175
 Pro Ala Gln Leu Lys Ala Gly Glu Met Asn His Phe Ser Phe Asp Lys
 180 185 190
 Val Glu Thr Tyr Ala Val Arg Ile Arg Met Val Lys Ala Asp Asn Lys
 195 200 205
 Arg Gly Thr Ser Ile Thr Glu Val Gln Ile Phe Ala Lys Gln Val Ala
 210 215 220

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Ala Ala Lys Gln Gly Gln Thr Arg Ile Gln Val Asp Gly Lys Asp Leu
 225 230 235 240
 Ala Asn Phe Asn Pro Asp Leu Thr Asp Tyr Tyr Leu Glu Ser Val Asp
 245 250 255
 Gly Lys Val Pro Ala Val Thr Ala Ser Val Ser Asn Asn Gly Leu Ala
 260 265 270
 Thr Val Val Pro Ser Val Arg Glu Gly Glu Pro Val Arg Val Ile Ala
 275 280 285
 Lys Ala Glu Asn Gly Asp Ile Leu Gly Glu Tyr Arg Leu His Phe Thr
 290 295 300
 Lys Asp Lys Ser Leu Leu Ser His Lys Pro Val Ala Ala Val Lys Gln
 305 310 315 320
 Ala Arg Leu Leu Gln Val Gly Gln Ala Leu Glu Leu Pro Thr Lys Val
 325 330 335
 Pro Val Tyr Phe Thr Gly Lys Asp Gly Tyr Glu Thr Lys Asp Leu Thr
 340 345 350
 Val Glu Trp Glu Glu Val Pro Ala Glu Asn Leu Thr Lys Ala Gly Gln
 355 360 365
 Phe Thr Val Arg Gly Arg Val Leu Gly Ser Asn Leu Val Ala Glu Ile
 370 375 380
 Thr Val Arg Val Thr Asp Lys Leu Gly Glu Thr Leu Ser Asp Asn Pro
 385 390 395 400
 Asn Tyr Asp Glu Asn Ser Asn Gln Ala Phe Ala Ser Ala Thr Asn Asp
 405 410 415
 Ile Asp Lys Asn Ser His Asp Arg Val Asp Tyr Leu Asn Asp Gly Asp
 420 425 430
 His Ser Glu Asn Arg Arg Trp Thr Asn Trp Ser Pro Thr Pro Ser Ser
 435 440 445
 Asn Pro Glu Val Ser Ala Gly Val Ile Phe Arg Glu Asn Gly Lys Ile
 450 455 460
 Val Glu Arg Thr Val Thr Gln Gly Lys Val Gln Phe Phe Ala Asp Ser
 465 470 475 480
 Gly Thr Asp Ala Pro Ser Lys Leu Val Leu Glu Arg Tyr Val Gly Pro
 485 490 495
 Glu Phe Glu Val Pro Thr Tyr Tyr Ser Asn Tyr Gln Ala Tyr Asp Ala
 500 505 510
 Asp His Pro Phe Asn Asn Pro Glu Asn Trp Glu Ala Val Pro Tyr Arg
 515 520 525
 Ala Asp Lys Asp Ile Ala Ala Gly Asp Glu Ile Asn Val Thr Phe Lys
 530 535 540
 Ala Ile Lys Ala Lys Ala Met Arg Trp Arg Met Glu Arg Lys Ala Asp
 545 550 555 560

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Lys Ser Gly Val Ala Met Ile Glu Met Thr Phe Leu Ala Pro Ser Glu
 565 570 575
 Leu Pro Gln Glu Ser Thr Gln Ser Lys Ile Leu Val Asp Gly Lys Glu
 580 585 590
 Leu Ala Asp Phe Ala Glu Asn Arg Gln Asp Tyr Gln Ile Thr Tyr Lys
 595 600 605
 Gly Gln Arg Pro Lys Val Ser Val Glu Glu Asn Asn Gln Val Ala Ser
 610 615 620
 Thr Val Val Asp Ser Gly Glu Asp Ser Phe Pro Val Leu Val Arg Leu
 625 630 635 640
 Val Ser Glu Ser Gly Lys Gln Val Lys Glu Tyr Arg Ile His Leu Thr
 645 650 655
 Lys Glu Lys Pro Val Ser Glu Lys Thr Val Ala Ala Val Gln Glu Asp
 660 665 670
 Leu Pro Lys Ile Glu Phe Val Glu Lys Asp Leu Ala Tyr Lys Thr Val
 675 680 685
 Glu Lys Lys Asp Ser Thr Leu Tyr Leu Gly Glu Thr Arg Val Glu Gln
 690 695 700
 Glu Gly Lys Val Gly Lys Glu Arg Ile Phe Thr Ala Ile Asn Pro Asp
 705 710 715 720
 Gly Ser Lys Glu Glu Lys Leu Arg Glu Val Val Glu Val Pro Thr Asp
 725 730 735
 Arg Ile Val Leu Val Gly Thr Lys Pro Val Ala Gln Glu Ala Lys Lys
 740 745 750
 Pro Gln Val Ser Glu Lys Ala Asp Thr Lys Pro Ile Asp Ser Ser Glu
 755 760 765
 Ala Ser Gln Thr Asn Lys Ala Gln
 770 775

(2) INFORMATION FOR SEQ ID NO: 87:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 133 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

CTATCACTAT GTAAATAAG AGATTATTC ACAAGAAGCT AAAGATTAA TTCAGACAGG 60
 AAAGCCTGAC AGGAATGAAG TTGTATATGG TTTGGTGTAT CAAAAGATC AGTTGCCTCA 120
 AACAGGGACA GAA 133

(2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

Tyr	His	Tyr	Val	Asn	Lys	Glu	Ile	Ile	Ser	Gln	Glu	Ala	Lys	Asp	Leu
1				5					10					15	
Ile	Gln	Thr	Gly	Lys	Pro	Asp	Arg	Asn	Glu	Val	Val	Tyr	Gly	Leu	Val
			20					25					30		
Tyr	Gln	Lys	Asp	Gln	Leu	Pro	Gln	Thr	Gly	Thr	Glu				
			35				40								

(2) INFORMATION FOR SEQ ID NO: 89:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 775 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

TGAGACTCCT	CAATCAATAA	CAAATCAGGA	GCAAGCTAGG	ACAGAAAACC	AAGTAGTAGA	60
GACAGAGGAA	GCTCCAAAAG	AAGAAGCACC	TAAACACGAA	GAAAGTCCAA	AGGAAGAACC	120
AAAATCGGAG	GTAACACCTA	CTGACGACAC	CCTTCCTAAA	GTAGAAGAGG	GGARAAGAAG	180
TTCAGCAGAA	CCAGCTCCAG	TTGAAGAAGT	AGGTGGAGAA	GTGAGTCAA	AACCAGAGGA	240
AAAAGTAGCA	GTTAAGCCAG	AAAGTCAACC	ATCAGACAAA	CCAGCTGAGG	AATCAAAAGT	300
TGAACAAGCA	GGTGAACCGA	TCGCGCCAAG	AGAAGACGAA	AAGGCACCAG	TCGAGCCAGA	360
AAAGCAACCA	GAAGTCTCTG	AAGAAGAGAA	GGCTGTAGAG	GAACACCCGA	AACAAGAAGA	420
GTCAACTCCA	GATACCAAGG	CTGAAGAAAC	TGTAGAACCA	AAAGAGGAGA	CTGTTAATCA	480
ATCTATTGAA	CAACCAAAAAG	TTGAAACGCC	TGCTGTAGAA	AAACAACACG	AACCAACAGA	540
GGAACCAAAA	GTTGAACAAG	CAGGTGAACC	AGTCGCGCCA	AGAGAAGACG	AACAGGCACC	600
AACGSCACCA	GTTGAGCCAG	AAAAGCAACC	AGAAGTTCCT	GAAGAAGAGA	AGGCTGTAGA	660
GGAACACCCG	AAACCAGAAG	ATAAAATAAA	GGGTATTGGT	ACTAAAGAAC	CAGTTGATAA	720
AAGTGAGTTA	AATAATCAAA	TTGATAAAGC	TAGTTCAGTT	TCTCCTACTG	ATTAT	775

(2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 258 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single

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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

Glu Thr Pro Gln Ser Ile Thr Asn Gln Glu Gln Ala Arg Thr Glu Asn
 1 5 10 15
 Gln Val Val Glu Thr Glu Glu Ala Pro Lys Glu Glu Ala Pro Lys Thr
 20 25 30
 Glu Glu Ser Pro Lys Glu Glu Pro Lys Ser Glu Val Lys Pro Thr Asp
 35 40 45
 Asp Thr Leu Pro Lys Val Glu Gly Lys Glu Asp Ser Ala Glu Pro
 50 55 60
 Ala Pro Val Glu Glu Val Gly Gly Glu Val Glu Ser Lys Pro Glu Glu
 65 70 75 80
 Lys Val Ala Val Lys Pro Glu Ser Gln Pro Ser Asp Lys Pro Ala Glu
 85 90 95
 Glu Ser Lys Val Glu Gln Ala Gly Glu Pro Val Ala Pro Arg Glu Asp
 100 105 110
 Glu Lys Ala Pro Val Glu Pro Glu Lys Gln Pro Glu Ala Pro Glu Glu
 115 120 125
 Glu Lys Ala Val Glu Glu Thr Pro Lys Gln Glu Glu Ser Thr Pro Asp
 130 135 140
 Thr Lys Ala Glu Glu Thr Val Glu Pro Lys Glu Glu Thr Val Asn Gln
 145 150 155 160
 Ser Ile Glu Gln Pro Lys Val Glu Thr Pro Ala Val Glu Lys Gln Thr
 165 170 175
 Glu Pro Thr Glu Glu Pro Lys Val Glu Gln Ala Gly Glu Pro Val Ala
 180 185 190
 Pro Arg Glu Asp Glu Gln Ala Pro Thr Ala Pro Val Glu Pro Glu Lys
 195 200 205
 Gln Pro Glu Val Pro Glu Glu Glu Lys Ala Val Glu Thr Pro Lys
 210 215 220
 Pro Glu Asp Lys Ile Lys Gly Ile Gly Thr Lys Glu Pro Val Asp Lys
 225 230 235 240
 Ser Glu Leu Asn Asn Gln Ile Asp Lys Ala Ser Ser Val Ser Pro Thr
 245 250 255
 Asp Tyr

(2) INFORMATION FOR SEQ ID NO: 91:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 199 base pairs

(B) TYPE: nucleic acid

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

(2) INFORMATION FOR SEQ ID NO:92:

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

(2) INFORMATION FOR SEQ ID NO: 93:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

CGACAAAGGT GAGACTGAGG TTCAACCAGA GTCGCCAGAT ACTGTGGTAA GTGATAAAGG	60
TGAACCAGAG CAGGTAGCAC CGCTTCCAGA ATATAAGGGT AATATTGAGC AAGTAAACC	120
TGAAACTCCG GTTGAGAAGA CCAAGAACA AGGTCCAGAA AAAACTGAAG AAGTTCAGT	180
AAAACCAACA GAAGAAACAC CAGTAAATCC AATGAAGT ACTACAGAAG GAACCTCAAT	240

TCAAGAAGCA GAAATCCAG TTCAACCTGC AGAAGAATCA ACAACGAATT CAGAGAAAGT 300
 ATCACCAGAT ACATCTAGCA AAAATACTGG GGAAGTGTCC AGTAATCCTA GTGATTCGAC 360
 AACCTCAGTT GGAGAATCAA ATAAACCAGA ACATAATGAC TCTAAAAATG AAAATTCAGA 420
 AAAAAGTGTG GAAGAAGTTC CAGTAAATCC AAATGAAGGC ACAGTAGAAG GTACCTCATA 480
 TCAAGAAACA GAAAAACCAG TTCAACCTGC AGAAGAAACA CAAACAAAT CTGGGAAAT 540
 AGCTAACGAA AATACTGGAG AAGTATCCAA TAAACCTAGT GATTCAAAAC CACCAATTGA 600
 AGAATCAAAT CAACCAGAAA AAAACGGAAC TGCAACAAAA CCAGAAAATT CAGGTAATAC 660
 AACATCAGAG AATGGACAAA CAGAACCAGA ACCATCAAAC GGAAATTCAA CTGAGGATGT 720
 TTCAACCGAA TCAACACAT CCAATTCAAA TGGAACGAA GAAATTAAAC AAGAAAATGA 780
 ACTAGACCTT GATAAAAAGG TAGAAGAACC AGAGAAAACA CTTGAATTAA GAAAT 835

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 278 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

Asp Lys Gly Glu Thr Glu Val Gln Pro Glu Ser Pro Asp Thr Val Val
 1 5 10 15
 Ser Asp Lys Gly Glu Pro Glu Gln Val Ala Pro Leu Pro Glu Tyr Lys
 20 25 30
 Gly Asn Ile Glu Gln Val Lys Pro Glu Thr Pro Val Glu Lys Thr Lys
 35 40 45
 Glu Gln Gly Pro Glu Lys Thr Glu Glu Val Pro Val Lys Pro Thr Glu
 50 55 60
 Glu Thr Pro Val Asn Pro Asn Glu Gly Thr Thr Glu Gly Thr Ser Ile
 65 70 75 80
 Gln Glu Ala Glu Asn Pro Val Gln Pro Ala Glu Glu Ser Thr Thr Asn
 85 90 95
 Ser Glu Lys Val Ser Pro Asp Thr Ser Ser Lys Asn Thr Gly Glu Val
 100 105 110
 Ser Ser Asn Pro Ser Asp Ser Thr Thr Ser Val Gly Glu Ser Asn Lys
 115 120 125
 Pro Glu His Asn Asp Ser Lys Asn Glu Asn Ser Glu Lys Thr Val Glu
 130 135 140
 Glu Val Pro Val Asn Pro Asn Glu Gly Thr Val Glu Gly Thr Ser Asn
 145 150 155 160

Gln Glu Thr Glu Lys Pro Val Gln Pro Ala Glu Glu Thr Gln Thr Asn
165 170 175

Ser Gly Lys Ile Ala Asn Glu Asn Thr Gly Glu Val Ser Asn Lys Pro
180 185 190

Ser Asp Ser Lys Pro Pro Val Glu Glu Ser Asn Gln Pro Glu Lys Asn
195 200 205

Gly Thr Ala Thr Lys Pro Glu Asn Ser Gly Asn Thr Thr Ser Glu Asn
210 215 220

Gly Gln Thr Glu Pro Glu Pro Ser Asn Gly Asn Ser Thr Glu Asp Val
225 230 235 240

Ser Thr Glu Ser Asn Thr Ser Asn Ser Asn Gly Asn Glu Glu Ile Lys
245 250 255

Gln Glu Asn Glu Leu Asp Pro Asp Lys Lys Val Glu Glu Pro Glu Lys
260 265 270

Thr Leu Glu Leu Arg Asn
275

(2) INFORMATION FOR SEQ ID NO: 95:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 709 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

AAATCAATTG GTAGCACAAAG ATCCAAAAGC ACAAGATAGC ACTAAACTGA CTGCTGAAAA 60

ATCAACTGTT AAAGCACCTG CTCAAAGAGT AGATGTAATA GATATAACTC ATTTAACAGA 120

TGAAGAAAAA GTTAAGGTTG CTATTTTACA AGCAAATGGT TCAGCATTAG ACGGAGCGAC 180

AATCAATGTA GCTGGAGATG GTACAGCAAC AATCACATTC CCAGATGGTT CAGTAGTGAC 240

GATTCTAGGA AAAGATACAG TTCAACAATC TGCAGAAAGT GAATCTGTAA CTCAGAAGC 300

TACACCAGAG TATAAGCTAG AAAATACACC AGGTGGAGAT AAGGGAGGCA ATACTGGAAG 360

CTCAGATGCT AATGCCAATG AAGGCGGTGG TAGCCAGGCG GGTGGATCAG CTCACACAGG 420

TTCAAAAAAC TCAGTCTAAT CACAAGCTTC TAAGCAATTA GCTACTGAAA AGAATCAGC 480

TAAAAATGCC ATTGAAAAAG CAGCCAAGGA CAAGCAGGAT GAAATCAAAG GCGCACCCT 540

TTCTGATAAA GAAAAAGCAG AACTTTTAGC AAGAGTGGAA GCAGAAAAAC AAGCAGCTCT 600

CAAAGAGATT GAAATGCGA AAACATATGA AGATGTGAAG GAAGCAGAAA CGATTGGAGT 660

GCAAGCCATT GCCATGGTTA CAGTTCCTAA GAGACCAAGT GCTCCTAAT 709

(2) INFORMATION FOR SEQ ID NO:96:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 236 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

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Asn Gln Leu Val Ala Gln Asp Pro Lys Ala Gln Asp Ser Thr Lys Leu
 1             5             10             15

Thr Ala Glu Lys Ser Thr Val Lys Ala Pro Ala Gln Arg Val Asp Val
20             25             30

Lys Asp Ile Thr His Leu Thr Asp Glu Glu Lys Val Lys Val Ala Ile
35             40             45

Leu Gln Ala Asn Gly Ser Ala Leu Asp Gly Ala Thr Ile Asn Val Ala
50             55             60

Gly Asp Gly Thr Ala Thr Ile Thr Phe Pro Asp Gly Ser Val Val Thr
65             70             75             80

Ile Leu Gly Lys Asp Thr Val Gln Gln Ser Ala Lys Gly Glu Ser Val
85             90             95

Thr Gln Glu Ala Thr Pro Glu Tyr Lys Leu Glu Asn Thr Pro Gly Gly
100            105            110

Asp Lys Gly Gly Asn Thr Gly Ser Ser Asp Ala Asn Ala Asn Glu Gly
115            120            125

Gly Gly Ser Gln Ala Gly Gly Ser Ala His Thr Gly Ser Gln Asn Ser
130            135            140

Ala Gln Ser Gln Ala Ser Lys Gln Leu Ala Thr Glu Lys Glu Ser Ala
145            150            155            160

Lys Asn Ala Ile Glu Lys Ala Ala Lys Asp Lys Gln Asp Glu Ile Lys
165            170            175

Gly Ala Pro Leu Ser Asp Lys Glu Lys Ala Glu Leu Leu Ala Arg Val
180            185            190

Glu Ala Glu Lys Gln Ala Ala Leu Lys Glu Ile Glu Asn Ala Lys Thr
195            200            205

Met Glu Asp Val Lys Glu Ala Glu Thr Ile Gly Val Gln Ala Ile Ala
210            215            220

Met Val Thr Val Pro Lys Arg Pro Val Ala Pro Asn
225            230            235

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(2) INFORMATION FOR SEQ ID NO: 97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 787 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

CAAACAGTCA GCTTCAGGAA CGATTGAGGT GATTTCACGA GAAATGGCT CTGGGACACG	60
GGGTGCCTTC ACAGAAATCA CAGGGATTCT CAAAAAGAC GGTGATAAAA AAATTGACAA	120
CACTGCCAAA ACAGCTGTGA TTCAAAATAG TACAGAAGGT GTTCTCTCAG CAGTTCAAGG	180
GAATGCTAAT GCTATCGGCT ACATCTCCTT GGGATCTTTA ACGAAATCTG TCAAGGCTTT	240
AGAGATTGAT GGTGTCAAGG CTAGTCGAGA CACAGTTTGA GATGGTGAAT ACCCTCTTCA	300
ACGTCCCTTC AACATTGTTT GGTCTTCTAA TCTTTCCAAG CTAGGTCAAG ATTTTATCAG	360
CTTTATCCAC TCCAAACAAG GTCAACAAGT GGTACAGAT AATAAATTTA TTGAAGCTAA	420
AACCGAAACC ACGGAATATA CAAGCCAACA CTTATCAGGC AAGTTGTCTG TTGTAGGTTT	480
CACTTCAGTA TCTCTTTTAA TGGAAAAATT AGCAGAAGCT TATAAAAAAG AAAATCCAGA	540
AGTTACGATT GATATTACCT CTAATGGGTC TTCAGCAGGT ATTACCGCTG TTAAGGAGAA	600
AACCGCTGAT ATTGGTATGG TTTCTAGGGA ATTAACCTCT GAAGAAGGTA AGAGTCTCAC	660
CCATGATGCT ATTGCTTTAG ACGGTATTGC TGTGTGTGTC AATAATGACA ATAAGGCAAG	720
CCAAGTCAGT ATGGCTGAAC TTGCAGACGT TTTAGTGGC AAATTAACCA CCTGGGACAA	780
GATTAAA	787

(2) INFORMATION FOR SEQ ID NO:98:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 262 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

Lys	Gln	Ser	Ala	Ser	Gly	Thr	Ile	Glu	Val	Ile	Ser	Arg	Glu	Asn	Gly
1				5					10					15	
Ser	Gly	Thr	Arg	Gly	Ala	Phe	Thr	Glu	Ile	Thr	Gly	Ile	Leu	Lys	Lys
			20					25					30		
Asp	Gly	Asp	Lys	Lys	Ile	Asp	Asn	Thr	Ala	Lys	Thr	Ala	Val	Ile	Gln
			35				40					45			
Asn	Ser	Thr	Glu	Gly	Val	Leu	Ser	Ala	Val	Gln	Gly	Asn	Ala	Asn	Ala
			50				55				60				
Ile	Gly	Tyr	Ile	Ser	Leu	Gly	Ser	Leu	Thr	Lys	Ser	Val	Lys	Ala	Leu
65				70					75					80	
Glu	Ile	Asp	Gly	Val	Lys	Ala	Ser	Arg	Asp	Thr	Val	Leu	Asp	Gly	Glu
				85					90					95	

Tyr Pro Leu Gln Arg Pro Phe Asn Ile Val Trp Ser Ser Asn Leu Ser
 100 105 110
 Lys Leu Gly Gln Asp Phe Ile Ser Phe Ile His Ser Lys Gln Gly Gln
 115 120 125
 Gln Val Val Thr Asp Asn Lys Phe Ile Glu Ala Lys Thr Glu Thr Thr
 130 135 140
 Glu Tyr Thr Ser Gln His Leu Ser Gly Lys Leu Ser Val Val Gly Ser
 145 150 155 160
 Thr Ser Val Ser Ser Leu Met Glu Lys Leu Ala Glu Ala Tyr Lys Lys
 165 170 175
 Glu Asn Pro Glu Val Thr Ile Asp Ile Thr Ser Asn Gly Ser Ser Ala
 180 185 190
 Gly Ile Thr Ala Val Lys Glu Lys Thr Ala Asp Ile Gly Met Val Ser
 195 200 205
 Arg Glu Leu Thr Pro Glu Glu Gly Lys Ser Leu Thr His Asp Ala Ile
 210 215 220
 Ala Leu Asp Gly Ile Ala Val Val Val Asn Asn Asp Asn Lys Ala Ser
 225 230 235 240
 Gln Val Ser Met Ala Glu Leu Ala Asp Val Phe Ser Gly Lys Leu Thr
 245 250 255
 Thr Trp Asp Lys Ile Lys
 260

(2) INFORMATION FOR SEQ ID NO: 99:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 421 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

ATTTCGATGAT GCGGATGAAA AGATGACCCG TGATGAAATT GCCTATATGC TGACAAATAG	60
TGAAGAARCA TTGGATGCTG ATGAGATTGA GATGCTACAA GGTGCTCTTT CGCTCGATGA	120
ACTGATGGCA CGAGAGGTTA TGGTTCCTCG AACGGATGCC TTTATGGTGG ATATTACGGA	180
TGATAGTCAA GCCATTATCC AAAGTATTTT AAAACAAAAA TATTCTCGTA TCCCGGTTTA	240
TGATGGGGAT AAGGACAATG TAATTGGAAT CATTACACCC AAGAGTCTCC TTAAGGCAGG	300
CTTTGTGGAC GGTTTTGACA ATATTGTTTG GAAGAGAATT TTACAAGATC CACTTTTGTG	360
ACCTGAAACT ATTTTGTGG ATGACTTGCT AAAAGAAGCT CGAAATACCC AAAGACAAAT	420
G	421

(2) INFORMATION FOR SEQ ID NO:100:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 140 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

```

Phe Asp Asp Ala Asp Glu Lys Met Thr Arg Asp Glu Ile Ala Tyr Met
 1             5             10             15
Leu Thr Asn Ser Glu Glu Thr Leu Asp Ala Asp Glu Ile Glu Met Leu
          20             25             30
Gln Gly Val Phe Ser Leu Asp Glu Leu Met Ala Arg Glu Val Met Val
          35             40             45
Pro Arg Thr Asp Ala Phe Met Val Asp Ile Gln Asp Asp Ser Gln Ala
          50             55             60
Ile Ile Gln Ser Ile Leu Lys Gln Asn Tyr Ser Arg Ile Pro Val Tyr
 65             70             75             80
Asp Gly Asp Lys Asp Asn Val Ile Gly Ile Ile His Thr Lys Ser Leu
          85             90             95
Leu Lys Ala Gly Phe Val Asp Gly Phe Asp Asn Ile Val Trp Lys Arg
          100            105            110
Ile Leu Gln Asp Pro Leu Phe Val Pro Glu Thr Ile Phe Val Asp Asp
          115            120            125
Leu Leu Lys Glu Leu Arg Asn Thr Gln Arg Gln Met
          130            135            140

```

(2) INFORMATION FOR SEQ ID NO: 101:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 331 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

```

GGAGAGTCGA TCAAAGTAG ATGAAGCTGT GTCTAAGTTT GAAAAGGACT CATCTTCTTC      60
GTCAAGTTCA GACTCTTCCA CTAAACCGGA AGCTTCAGAT ACAGCGAAGC CAAACAAGCC      120
GACAGAACCA GGAGAAAAGG TAGCAGAAGC TAAGAAGAAG GTTGAAGAAG CTGAGAAAAA      180
AGCCAAGGAT CAAAAGAAG AAGATCGTCG TAACTACCCA ACCATTACTT ACAAACGCT      240
TGAAGTTGAA ATTGCTGAGT CCGATGTGGA AGTTAAAAA GCGGAGCTTG AACTAGTAAA      300
AGTGAAAGCT AACGAACCTC GAGACGAGCA A                                     331

```

(2) INFORMATION FOR SEQ ID NO:102:

0076527.01204

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 110 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

```

Glu Ser Arg Ser Lys Val Asp Glu Ala Val Ser Lys Phe Glu Lys Asp
1          5          10          15

Ser Ser Ser Ser Ser Ser Ser Asp Ser Ser Thr Lys Pro Glu Ala Ser
20          25          30

Asp Thr Ala Lys Pro Asn Lys Pro Thr Glu Pro Gly Glu Lys Val Ala
35          40          45

Glu Ala Lys Lys Lys Val Glu Glu Ala Glu Lys Lys Ala Lys Asp Gln
50          55          60

Lys Glu Glu Asp Arg Arg Asn Tyr Pro Thr Ile Thr Tyr Lys Thr Leu
65          70          75          80

Glu Leu Glu Ile Ala Glu Ser Asp Val Glu Val Lys Lys Ala Glu Leu
85          90          95

Glu Leu Val Lys Val Lys Ala Asn Glu Pro Arg Asp Glu Gln
100         105         110

```

(2) INFORMATION FOR SEQ ID NO: 103:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 358 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

```

ATGGACAACA GGAACTGGG ACGAGGTTAT ATCTGGTAAG ATTGACAAGT ACAAGATCC      60
AGATATTCCA ACAGTTGAAT CACAAGAAGT TACGTCAGAC TCTAGTGATA AAGAAATAAC      120
GGTAAGGTAT GACCGTTTAT CAACACCAGA AAAACCAATC CCACAACCAA ATCCAGAGCA      180
TCCAAGTGT CCGACACCAA ACCCAGAACT ACCAAATCAA GAGACTCCAA CACCAGATAA      240
ACCAACTCCA GAACCAGGTA CTCCAAAAAC TGAAACTCCA GTGAATCCAG ACCCAGAAGT      300
TCGACTTAT GAGACAGGTA AGAGAGAGGA ATTGCCAAC ACAGGTACAG AAGCTAAT      358

```

(2) INFORMATION FOR SEQ ID NO:104:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 119 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single

09755272.012201

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

Trp Thr Thr Gly Asn Trp Asp Glu Val Ile Ser Gly Lys Ile Asp Lys
 1 5 10 15
 Tyr Lys Asp Pro Asp Ile Pro Thr Val Glu Ser Gln Glu Val Thr Ser
 20 25 30
 Asp Ser Ser Asp Lys Glu Ile Thr Val Arg Tyr Asp Arg Leu Ser Thr
 35 40 45
 Pro Glu Lys Pro Ile Pro Gln Pro Asn Pro Glu His Pro Ser Val Pro
 50 55 60
 Thr Pro Asn Pro Glu Leu Pro Asn Gln Glu Thr Pro Thr Pro Asp Lys
 65 70 75 80
 Pro Thr Pro Glu Pro Gly Thr Pro Lys Thr Glu Thr Pro Val Asn Pro
 85 90 95
 Asp Pro Glu Val Pro Thr Tyr Glu Thr Gly Lys Arg Glu Glu Leu Pro
 100 105 110
 Asn Thr Gly Thr Glu Ala Asn
 115

(2) INFORMATION FOR SEQ ID NO: 105:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1879 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

CGATGGGCTC AATCCAACCC CAGGTCAAGT CTTACCTGAA GAGACATCGG GAACGAAAGA 60
 GGGTGACTTA TCAGAAAAAC CAGGAGACAC CGTTCTCACT CAAGCGAAAC CTGAGGGCGT 120
 TACTGGAAT ACGAATTCAC TTCCGACACC TACAGAAAGA ACTGAAGTGA GCGAGGAAAC 180
 AAGCCCTTCT AGTCTGGATA CACTTTTIGA AAAAGATGAA GAAGCTCAA AAAATCCAGA 240
 GCTAACAGAT GTCTTAAAG AAAGTGTAGA TACAGCTGAT GTGGATGGGA CACAAGCAAG 300
 TCCAGCAGAA ACTACTCCTG AACAAGTAAA AGGTGGAGTG AAAGAAAATA CAAAAGACAG 360
 CATCGATGTT CCTCTGCTT ATCTTGAAAA AGCTGAAGGG AAAGTCTCTT TCACGTGCCG 420
 TGTAACCAA GTAATTCCTT ATGAACTATT CGCTGGTGAT GGTATGTAA CTCGCTATT 480
 ACTAAAAGCT TCGGATAATG CTCCTTGGTC TGACAATGGT ACTGCTAAAA ATCCTGCTTT 540
 ACCCTCTCTT GAAGGATTAA CAAAAGGGAA ATACTTCTAT GAAGTAGACT TAAATGGCAA 600

0076527.012004

TACTGTTGGT AAACAAGGTC AAGCTTTAAT TGATCAACTT CGCGCTAATG GTACTCAAAC 660
 TTATAAAGCT ACTGTTAAAG TTTACGGAAA TAAAGACGGT AAAGCTGACT TGAATATCT 720
 AGTTGCTACT AAAAATGTAG ACATCAACAT CAATGGATTA GTTGCTAAAG AAACAGTTCA 780
 AAAAGCCGTT GCAGACAACG TTAAGACAG TATCGATGTT CCAGCAGCCT ACCTAGAAAA 840
 AGCCAAGGGT GAAGGTCCAT TCACAGCAGG TGTCAACCAT GTGATTCCAT ACGAATCTTT 900
 CGCAGGTGAT GGCATGTTGA CTCGTCTCTT GCTCAAGGCA TCTGACAAGG CACCATTGGTC 960
 AGATAACGGC GACGCTAAAA ACCCAGCCCT ATCTCCACTA GGCGAAAACG TGAAGACCAA 1020
 AGGTCAATAC TTCTATCAAN TAGCCTTGGA CGGAAATGTA GCTGGCAAAG AAAAACAAGC 1080
 GCTCATTGAC CAGTTCGGAG CAAANGGTAC TCAAACCTAC AGCGCTACAG TCAATGTCTA 1140
 TGGAACAAA GACGGTAAAC CAGACTTGGA CAACATCGTA GCAACTAAAA AAGTCACTAT 1200
 TAACATAAAC GGTTAATTT CTAAGAAAA AGTTCAAAAA GCCGTTGCAG ACAACGTTAA 1260
 NGACAGTATC GATGTTCCAG CAGCCTACCT AGAAAAAGCC AAGGGTGAAG GTCCATTAC 1320
 AGCAGGTGTC AACCATGIGA TTCCATACGA ACTCTTCGCA GGTGATGGTA TGTGTGACTCG 1380
 TCTCTTGCTC AAGGCATCTG ACAAGGCACC ATGSTCAGAT AACGNGACG CTAACAAACC 1440
 AGCNCATATC CCACTAGGTG AAAACGTGAA GACCAAAGGT CAATACTTCT ATCAANTAGC 1500
 CTTGGACGGA AATGTAGCTG GCAAAGAAAA ACAAGCGCTC ATTGACCACT TCCGAGCAAA 1560
 CGGTACTCAA ACTTACAGCG CTACAGTCAA TGTCTATGGT AACAAAGACG GTAAACCAGA 1620
 CTTGGACAAC ATCGTAGCAA CTAACAAAAGT CACTATTAAAG ATAAATGTTA AAGAAACATC 1680
 AGACACAGCA AATGGTTCAT TATCACCTTC TAACTCTGGT TCTGGCGTGA CTCCGATGAA 1740
 TCACAATCAT GCTACAGGTA CTACAGATAG CATGCCTGCT GACACCATGA CAAGTTCTAC 1800
 CAACACGATG GCAGGTGAAA ACATGGCTGC TTCTGCTAAC AAGATGTCTG ATACGATGAT 1860
 GTCAGAGGAT AAAGCTATG 1879

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 626 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

Asp Gly Leu Asn Pro Thr Pro Gly Gln Val Leu Pro Glu Glu Thr Ser
 1 5 10 15
 Gly Thr Lys Glu Gly Asp Leu Ser Glu Lys Pro Gly Asp Thr Val Leu
 20 25 30

Thr Gln Ala Lys Pro Glu Gly Val Thr Gly Asn Thr Asn Ser Leu Pro
 35 40 45
 Thr Pro Thr Glu Arg Thr Glu Val Ser Glu Glu Thr Ser Pro Ser Ser
 50 55 60
 Leu Asp Thr Leu Phe Glu Lys Asp Glu Glu Ala Gln Lys Asn Pro Glu
 65 70 75 80
 Leu Thr Asp Val Leu Lys Glu Thr Val Asp Thr Ala Asp Val Asp Gly
 85 90 95
 Thr Gln Ala Ser Pro Ala Glu Thr Thr Pro Glu Gln Val Lys Gly Gly
 100 105 110
 Val Lys Glu Asn Thr Lys Asp Ser Ile Asp Val Pro Ala Ala Tyr Leu
 115 120 125
 Glu Lys Ala Glu Gly Lys Gly Pro Phe Thr Ala Gly Val Asn Gln Val
 130 135 140
 Ile Pro Tyr Glu Leu Phe Ala Gly Asp Gly Met Leu Thr Arg Leu Leu
 145 150 155 160
 Leu Lys Ala Ser Asp Asn Ala Pro Trp Ser Asp Asn Gly Thr Ala Lys
 165 170 175
 Asn Pro Ala Leu Pro Pro Leu Glu Gly Leu Thr Lys Gly Lys Tyr Phe
 180 185 190
 Tyr Glu Val Asp Leu Asn Gly Asn Thr Val Gly Lys Gln Gly Gln Ala
 195 200 205
 Leu Ile Asp Gln Leu Arg Ala Asn Gly Thr Gln Thr Tyr Lys Ala Thr
 210 215 220
 Val Lys Val Tyr Gly Asn Lys Asp Gly Lys Ala Asp Leu Thr Asn Leu
 225 230 235 240
 Val Ala Thr Lys Asn Val Asp Ile Asn Ile Asn Gly Leu Val Ala Lys
 245 250 255
 Glu Thr Val Gln Lys Ala Val Ala Asp Asn Val Lys Asp Ser Ile Asp
 260 265 270
 Val Pro Ala Ala Tyr Leu Glu Lys Ala Lys Gly Glu Gly Pro Phe Thr
 275 280 285
 Ala Gly Val Asn His Val Ile Pro Tyr Glu Leu Phe Ala Gly Asp Gly
 290 295 300
 Met Leu Thr Arg Leu Leu Leu Lys Ala Ser Asp Lys Ala Pro Trp Ser
 305 310 315 320
 Asp Asn Gly Asp Ala Lys Asn Pro Ala Leu Ser Pro Leu Gly Glu Asn
 325 330 335
 Val Lys Thr Lys Gly Gln Tyr Phe Tyr Gln Xaa Ala Leu Asp Gly Asn
 340 345 350
 Val Ala Gly Lys Glu Lys Gln Ala Leu Ile Asp Gln Phe Arg Ala Xaa
 355 360 365

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 102229660

Gly Thr Gln Thr Tyr Ser Ala Thr Val Asn Val Tyr Gly Asn Lys Asp
 370 375 380
 Gly Lys Pro Asp Leu Asp Asn Ile Val Ala Thr Lys Lys Val Thr Ile
 385 390 395 400
 Asn Ile Asn Gly Leu Ile Ser Lys Glu Thr Val Gln Lys Ala Val Ala
 405 410 415
 Asp Asn Val Xaa Asp Ser Ile Asp Val Pro Ala Ala Tyr Leu Glu Lys
 420 425 430
 Ala Lys Gly Glu Gly Pro Phe Thr Ala Gly Val Asn His Val Ile Pro
 435 440 445
 Tyr Glu Leu Phe Ala Gly Asp Gly Met Leu Thr Arg Leu Leu Leu Lys
 450 455 460
 Ala Ser Asp Lys Ala Pro Trp Ser Asp Asn Gly Asp Ala Lys Asn Pro
 465 470 475 480
 Ala Leu Ser Pro Leu Gly Glu Asn Val Lys Thr Lys Gly Gln Tyr Phe
 485 490 495
 Tyr Gln Xaa Ala Leu Asp Gly Asn Val Ala Gly Lys Glu Lys Gln Ala
 500 505 510
 Leu Ile Asp Gln Phe Arg Ala Asn Gly Thr Gln Thr Tyr Ser Ala Thr
 515 520 525
 Val Asn Val Tyr Gly Asn Lys Asp Gly Lys Pro Asp Leu Asp Asn Ile
 530 535 540
 Val Ala Thr Lys Lys Val Thr Ile Lys Ile Asn Val Lys Glu Thr Ser
 545 550 555 560
 Asp Thr Ala Asn Gly Ser Leu Ser Pro Ser Asn Ser Gly Ser Gly Val
 565 570 575
 Thr Pro Met Asn His Asn His Ala Thr Gly Thr Thr Asp Ser Met Pro
 580 585 590
 Ala Asp Thr Met Thr Ser Ser Thr Asn Thr Met Ala Gly Glu Asn Met
 595 600 605
 Ala Ala Ser Ala Asn Lys Met Ser Asp Thr Met Met Ser Glu Asp Lys
 610 615 620
 Ala Met
 625

(2) INFORMATION FOR SEQ ID NO: 107:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 593 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

TTCCAATCAA AACAGGCAG ATGGTAAACT CAATATCGTG ACAACCTTTT ACCCTGTCTA 60
 TGAATTACC AAGCAAGTCG CAGGAGATAC GGCTAATGTA GAACCTCTAA TCGGTGCTGG 120
 GACAGAACCT CATGAATACG AACCATCTGC CAAGGCAGTT GCCAAAATCC AAGATGCAGA 180
 TACCTTCGTT TATGAAAATG AAAACATGGA AACATGGGTA CCTAAATTGC TAGATACCTT 240
 GGATAAGAAA AAAGTAAAA CCATCAAGGC GACAGGCGAT ATGTTGCTCT TGCCAGGTGG 300
 CGAGGAAGAA GAGGGAGACC ATGACCATGG AGAAGAAGGT CATCACCATG AGTTTGACCC 360
 CCATGTTTGG TTATCACCAG TTCGTGCCAT TAACTAGTA GAGCACCATC CGCGACACTT 420
 GTCAGCAGAT TATCCTGATA AAAAAGAGAC CTTTGAGAAG AATGCAGCTG CCTATATCGA 480
 AAAATTGCAA GCCTTGATA AGGCTTACGC AGAAGGTTTG TCTCAAGCAA AACAAAAGAG 540
 CTTTGTGACT CAACACGCAg CCTTTAACTa TCTTGCCTTG GACTATGGGA CTC 593

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

Ser Asn Gln Lys Gln Ala Asp Gly Lys Leu Asn Ile Val Thr Thr Phe
 1 5 10 15
 Tyr Pro Val Tyr Glu Phe Thr Lys Gln Val Ala Gly Asp Thr Ala Asn
 20 25 30
 Val Glu Leu Leu Ile Gly Ala Gly Thr Glu Pro His Glu Tyr Glu Pro
 35 40 45
 Ser Ala Lys Ala Val Ala Lys Ile Gln Asp Ala Asp Thr Phe Val Tyr
 50 55 60
 Glu Asn Glu Asn Met Glu Thr Trp Val Pro Lys Leu Leu Asp Thr Leu
 65 70 75 80
 Asp Lys Lys Lys Val Lys Thr Ile Lys Ala Thr Gly Asp Met Leu Leu
 85 90 95
 Leu Pro Gly Gly Glu Glu Glu Glu Gly Asp His Asp His Gly Glu Glu
 100 105 110
 Gly His His His Glu Phe Asp Pro His Val Trp Leu Ser Pro Val Arg
 115 120 125
 Ala Ile Lys Leu Val Glu His His Pro Arg His Leu Ser Ala Asp Tyr
 130 135 140
 Pro Asp Lys Lys Glu Thr Phe Glu Lys Asn Ala Ala Tyr Ile Glu
 145 150 155 160

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Lys Leu Gln Ala Leu Asp Lys Ala Tyr Ala Glu Gly Leu Ser Gln Ala
165 170 175

Lys Gln Lys Ser Phe Val Thr Gln His Ala Ala Phe Asn Tyr Leu Ala
180 185 190

Leu Asp Tyr Gly Thr
195

(2) INFORMATION FOR SEQ ID NO: 109:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1003 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

TATCACAGGA TCGACGGTA AGACAACCAC AACGACTATG ATTGGGGAAG TTTTGACTGC	60
TGCTGGCCAA CATGSTCTTT TATCAGGGAA TATCGGCTAT CCAGCTAGTC AGGTTGCTCA	120
AATAGCATCA GATAAGGACA CGCTTGTTAT GGAACCTTCT TCTTCCAAC TCATGGGTGT	180
TCAAGAATTC CATCCAGAGA TTGCGGTTAT TACCAACCTC ATGCCAACTC ATATCGACTA	240
CCATGGGTCA TTTTCGGAAT ATGTAGCAGC CAAGTGGAAT ATCCAGAACA AGATGACAGC	300
AGCTGATTTC CTGTCTTGA ACTTTAATCA AGACTTGCCA AAAGACTTGA CTTCCAAGAC	360
AGAAGCCACT GTTGACCAT TTTCAACACT TGAAAAGGTT GATGGAGCTT ATCTGGAAGA	420
TGGTCAACTC TACTCCGTG GTGAAGTAGT CATGGCAGCG AATGAAATCG GTGTCCAGG	480
TAGCCACAAT GTGGAAAATG CCCTTGCGAC TATTGCTGTA GCCAAGCTTC GTGATGTGGA	540
CAATCAAACC ATCAAGGAAA CTCCTTCAGC CTTGCGTGGT GTCAAACACC GTCTCCAGTT	600
TGTGGATGAC ATCAAGGGTG TTAATTTCTA TAACGACAGT AAATCAACTA ATATCTTGGC	660
TACTCAAAAA GCCTTGTCAG GATTTGACAA CAGCAAGGTC GTCTTGATTG CAGGTGGTTT	720
GGACCGTGCG AATGAGTTTG ACGAATTGGT GCCAGACATT ACTGGACTCA AGAAGATGGT	780
CATCTGGGT CAATCTGCAG AACGTGTCAA ACGGGCAGCA GACAAGGCTG GTGTCGCTTA	840
TGTGGAGGCG ACAGATATTG CAGATGCGAC CCGCAAGGCC TATGAGCTTG CGACTCAAGG	900
AGATGTGGTT CTCTTAGTC CTGCCAATGC TAGCTGGGAT ATGTATGCTA ACTTTGAAGT	960
ACGTGGCGAC CTCCTTATCG ACACAGTAGC GGAGTTAAAA GAA	1003

(2) INFORMATION FOR SEQ ID NO:110:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 335 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

Gly Ile Thr Gly Ser Asn Gly Lys Thr Thr Thr Thr Met Ile Gly
 1 5 10 15
 Glu Val Leu Thr Ala Ala Gly Gln His Gly Leu Leu Ser Gly Asn Ile
 20 25 30
 Gly Tyr Pro Ala Ser Gln Val Ala Gln Ile Ala Ser Asp Lys Asp Thr
 35 40 45
 Leu Val Met Glu Leu Ser Ser Phe Gln Leu Met Gly Val Gln Glu Phe
 50 55 60
 His Pro Glu Ile Ala Val Ile Thr Asn Leu Met Pro Thr His Ile Asp
 65 70 75 80
 Tyr His Gly Ser Phe Ser Glu Tyr Val Ala Lys Trp Asn Ile Gln
 85 90 95
 Asn Lys Met Thr Ala Ala Asp Phe Leu Val Leu Asn Phe Asn Gln Asp
 100 105 110
 Leu Ala Lys Asp Leu Thr Ser Lys Thr Glu Ala Thr Val Val Pro Phe
 115 120 125
 Ser Thr Leu Glu Lys Val Asp Gly Ala Tyr Leu Glu Asp Gly Gln Leu
 130 135 140
 Tyr Phe Arg Gly Glu Val Val Met Ala Ala Asn Glu Ile Gly Val Pro
 145 150 155 160
 Gly Ser His Asn Val Glu Asn Ala Leu Ala Thr Ile Ala Val Ala Lys
 165 170 175
 Leu Arg Asp Val Asp Asn Gln Thr Ile Lys Glu Thr Leu Ser Ala Phe
 180 185 190
 Gly Gly Val Lys His Arg Leu Gln Phe Val Asp Asp Ile Lys Gly Val
 195 200 205
 Lys Phe Tyr Asn Asp Ser Lys Ser Thr Asn Ile Leu Ala Thr Gln Lys
 210 215 220
 Ala Leu Ser Gly Phe Asp Asn Ser Lys Val Val Leu Ile Ala Gly Gly
 225 230 235 240
 Leu Asp Arg Gly Asn Glu Phe Asp Glu Leu Val Pro Asp Ile Thr Gly
 245 250 255
 Leu Lys Lys Met Val Ile Leu Gly Gln Ser Ala Glu Arg Val Lys Arg
 260 265 270
 Ala Ala Asp Lys Ala Gly Val Ala Tyr Val Glu Ala Thr Asp Ile Ala
 275 280 285
 Asp Ala Thr Arg Lys Ala Tyr Glu Leu Ala Thr Gln Gly Asp Val Val
 290 295 300
 Leu Leu Ser Pro Ala Asn Ala Ser Trp Asp Met Tyr Ala Asn Phe Glu

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305

310

315

320

Val Arg Gly Asp Leu Phe Ile Asp Thr Val Ala Glu Leu Lys Glu
 325 330 335

(2) INFORMATION FOR SEQ ID NO: 111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 412 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

AAGTTCATCG AAGATGGTTG GGAAGTCCAC TATATCGGGG ACAAGTGTGG TATCGAACAC 60
 CAAGAAATCC TTAAGTCAGG TTTGGATGTC ACCTTCCATT CTATTGCGAC TGGAAAATTTG 120
 CGTCGCTATT TCTCTTGGCA AATATGCTG GACGCTTTCA AAGTTGGTTG GGGAAATGTG 180
 CAATCGCTCT TTATCATGTT GCGACTGCGT CCACAGACCC TTTTTCAAA GGGGGGCTTT 240
 GTCTCAGTAC CGCCTGTTAT CGTCGCGCGT GTGTCAGGAG TGCCTGTCTT TATTCACGAA 300
 TCTGACCTGT CTATGGGCTT GGCCAATAAA ATCGCCTATA AATTGCGAC TAAGATGTAT 360
 TCAACCTTTG AACAAAGCTT GAGTTTGGCT AAGGTTGAGC ATGTGGGAGC GG 412

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

Ser Ser Ser Lys Met Val Gly Lys Ser Thr Ile Ser Gly Thr Ser Val
 1 5 10 15
 Val Ser Asn Thr Lys Lys Ser Leu Ser Gln Val Trp Met Ser Pro Ser
 20 25 30
 Ile Leu Leu Arg Leu Glu Asn Cys Val Ala Ile Ser Leu Gly Lys Ile
 35 40 45
 Cys Trp Thr Ser Ser Lys Leu Val Gly Glu Leu Ser Asn Arg Ser Leu
 50 55 60
 Ser Cys Cys Asp Cys Val His Arg Pro Phe Phe Gln Arg Gly Ala Leu
 65 70 75 80
 Ser Gln Tyr Arg Leu Leu Ser Leu Arg Val Cys Gln Glu Cys Leu Ser
 85 90 95
 Leu Phe Thr Asn Leu Thr Cys Leu Trp Ala Trp Pro Ile Lys Ser Pro

100

105

110

Ile Asn Leu Arg Leu Arg Cys Ile Gln Pro Leu Asn Lys Leu Arg Val
 115 120 125

Trp Leu Arg Leu Ser Met Trp Glu Arg
 130 135

(2) INFORMATION FOR SEQ ID NO: 113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 544 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

ATCGCTAGCT AGTGAAATGC AAGAAAGTAC ACGTAAATTC AAGGTTACTG CTGACCTAAC 60
 AGATGCCGGT GTTGAACGA TTGAAGTTCC TTGAGCATT GAAGATTTC CCAATGGGCT 120
 GACCGCTGTG GCGACTCCGC AAAAAATTAC AGTCAAGATT GGTAAGAAGG CTCAGAAGGA 180
 TAAGGTAAG ATTGTACCAG AGATTGACCC TAGTCAAATT GATAGTCGGG TACAAATTGA 240
 AAATGTGTCG GTGTCAGATA AAGAAAGTGC TATTACGAGT GACCAAGAGA CATTGGATAG 300
 AATTGATAAG ATTATCGCTG TTTTGCCAAC TAGCGAAGCT ATAACAGGTA ATTACAGTGG 360
 TTCAGTACCT TTGCAGGCAA TCGACCGCAA TGGTGTGTGC TTACCGGCAG TTACTACTCC 420
 GTTTGATACA ATAATGAAGG TGACTACAAA ACCAGTAGCA CCAAGTTCAA GCACATCAAA 480
 TTCAAGTACA AGCAGTTCAT CGGAGACATC TTCGTCAACG AAAGCAACTA GTTCAAAAAC 540
 GAAT 544

(2) INFORMATION FOR SEQ ID NO: 114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 181 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

Ser Leu Ala Ser Glu Met Gln Glu Ser Thr Arg Lys Phe Lys Val Thr
 1 5 10 15
 Ala Asp Leu Thr Asp Ala Gly Val Gly Thr Ile Glu Val Pro Leu Ser
 20 25 30
 Ile Glu Asp Leu Pro Asn Gly Leu Thr Ala Val Ala Thr Pro Gln Lys
 35 40 45
 Ile Thr Val Lys Ile Gly Lys Lys Ala Gln Lys Asp Lys Val Lys Ile

50	55	60
Val Pro Glu Ile Asp	Pro Ser Gln Ile Asp	Ser Arg Val Gln Ile Glu
65	70	75 80
Asn Val Met Val Ser Asp Lys	Glu Val Ser Ile Thr Ser Asp	Gln Glu
85	90	95
Thr Leu Asp Arg Ile Asp Lys	Ile Ile Ala Val Leu Pro Thr Ser Glu	
100	105	110
Arg Ile Thr Gly Asn Tyr Ser	Gly Ser Val Pro Leu Gln Ala Ile Asp	
115	120	125
Arg Asn Gly Val Val Leu Pro Ala Val Ile Thr	Pro Phe Asp Thr Ile	
130	135	140
Met Lys Val Thr Thr Lys Pro Val Ala Pro	Ser Ser Ser Thr Ser Asn	
145	150	155 160
Ser Ser Thr Ser Ser Ser Glu Thr Ser Ser	Ser Thr Lys Ala Thr	
165	170	175
Ser Ser Lys Thr Asn		
180		

(2) INFORMATION FOR SEQ ID NO: 115:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1267 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

GCACCAGATG GGGCACAAGG TTCAGGGATC AGATGTTGAA AAGTACTACT TTACCCAACG	60
CGGTCTTGAG CAGGCAGGAA TTACCATTCT TCCTTTTGAT GAAAAAATC TAGACGGTGA	120
TATGGAAATT ATCGCTGGAA ATGCCTTTCG TCCAGATAAC AACGTCGAAA TTGCCTATGC	180
GGACCAAAAT GGTATCAGCT ACAAACTGTA CCATGAGTTT CTAGGTAGCT TTATGCGTGA	240
CTTTGTTAGC ATGGGAGTAG CAGGAGCACA TGGAAAAACT TCAACGACAG GTATGTTGTC	300
TCATGTCTTG TTCTCACATTA CAGATACCAG CTTCTTGATT GGAGATGGGA CAGGTCGTGG	360
TTCGGCCAAT GCCAAATATT TTGCTTTGA ATCTGACGAA TATGAGCGTC ACTTCATGCC	420
TTACCAACCA GAATACTCTA TTATACCAA CATTGACTTT GACCATCCAG ATTATTTTCA	480
AAGTCTCGAG GATGTTTTTA ATGCCTTTAA CGACTATGCC AAACAAATCA CCAAGGGTCT	540
TTTTGTCTAT GGTGAAGATG CTGAATTGCG TAAGATTACG TCTGATGCAC CAATTATTAT	600
TTATGTTTTT GAAGCTGAAG GCAATGACTT TGTAAGTAGT GATCTTCTTC GTTCAATAAC	660
TGGTTCAACC TTCACCGTTC ATTTCCGTGG ACAAACCTTG GGGCAATTCC ACATTCCAAC	720
CTTTGGTTCG CACAATATCA TGAATGCGAC AGCCGTTATT GGTCTTCTTT ACACAGCAGG	780

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ATTTGATTG AACTTGGTGC GTGAGCACTT GAAACATTT GCCGGTGTTA AACGTCGTTT 840
 CACTGAGAAA ATGTCAATG ATACAGTGAT TATCGATGAC TTGCCCCACC ATCCAACAGA 900
 AATTATTGCG ACCTTGGATG CGGCTCGTCA GAAATACCCA AGCAAGGAAA TTGTAGCAGT 960
 CTTTCAACCG CATACCTTTA CAAGAACCAT TGCCTTGTGT GACGACTTTG CCCATGCTTT 1020
 AAACAAGCA GATGCTGTTT ATCTAGCGCA AATTTATGGC TCGGCTCGTG AAGTAGATCA 1080
 TGGTGACGTT AAGGTAGAAG ACCTAGCCAA CAAAATCAAC AAAAAACACC AAGTGATTAC 1140
 TGTGAAAAAT GTTCTCCAC TCCTAGACCA TGACAATGCT GTTTACGTCT TTATGGGAGC 1200
 AGGAGACATC CAAACCTATG AATACTCATT TGAGCGTCTC TTGTCTAACT TGACAAGCAA 1260
 TGTTCAA 1267

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 422 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

His Gln Met Gly His Lys Val Gln Gly Ser Asp Val Glu Lys Tyr Tyr
 1 5 10 15
 Phe Thr Gln Arg Gly Leu Glu Gln Ala Gly Ile Thr Ile Leu Pro Phe
 20 25 30
 Asp Glu Lys Asn Leu Asp Gly Asp Met Glu Ile Ile Ala Gly Asn Ala
 35 40 45
 Phe Arg Pro Asp Asn Asn Val Glu Ile Ala Tyr Ala Asp Gln Asn Gly
 50 55 60
 Ile Ser Tyr Lys Arg Tyr His Glu Phe Leu Gly Ser Phe Met Arg Asp
 65 70 75 80
 Phe Val Ser Met Gly Val Ala Gly Ala His Gly Lys Thr Ser Thr Thr
 85 90 95
 Gly Met Leu Ser His Val Leu Ser His Ile Thr Asp Thr Ser Phe Leu
 100 105 110
 Ile Gly Asp Gly Thr Gly Arg Gly Ser Ala Asn Ala Lys Tyr Phe Val
 115 120 125
 Phe Glu Ser Asp Glu Tyr Glu Arg His Phe Met Pro Tyr His Pro Glu
 130 135 140
 Tyr Ser Ile Ile Thr Asn Ile Asp Phe Asp His Pro Asp Tyr Phe Thr
 145 150 155 160
 Ser Leu Glu Asp Val Phe Asn Ala Phe Asn Asp Tyr Ala Lys Gln Ile

165 170 175
 Thr Lys Gly Leu Phe Val Tyr Gly Glu Asp Ala Glu Leu Arg Lys Ile
 180 185 190
 Thr Ser Asp Ala Pro Ile Tyr Tyr Tyr Gly Phe Glu Ala Glu Gly Asn
 195 200 205
 Asp Phe Val Ala Ser Asp Leu Leu Arg Ser Ile Thr Gly Ser Thr Phe
 210 215 220
 Thr Val His Phe Arg Gly Gln Asn Leu Gly Gln Phe His Ile Pro Thr
 225 230 235 240
 Phe Gly Arg His Asn Ile Met Asn Ala Thr Ala Val Ile Gly Leu Leu
 245 250 255
 Tyr Thr Ala Gly Phe Asp Leu Asn Leu Val Arg Glu His Leu Lys Thr
 260 265 270
 Phe Ala Gly Val Lys Arg Arg Phe Thr Glu Lys Ile Val Asn Asp Thr
 275 280 285
 Val Ile Ile Asp Asp Phe Ala His His Pro Thr Glu Ile Ile Ala Thr
 290 295 300
 Leu Asp Ala Ala Arg Gln Lys Tyr Pro Ser Lys Glu Ile Val Ala Val
 305 310 315 320
 Phe Gln Pro His Thr Phe Thr Arg Thr Ile Ala Leu Leu Asp Asp Phe
 325 330 335
 Ala His Ala Leu Asn Gln Ala Asp Ala Val Tyr Leu Ala Gln Ile Tyr
 340 345 350
 Gly Ser Ala Arg Glu Val Asp His Gly Asp Val Lys Val Glu Asp Leu
 355 360 365
 Ala Asn Lys Ile Asn Lys Lys His Gln Val Ile Thr Val Glu Asn Val
 370 375 380
 Ser Pro Leu Leu Asp His Asp Asn Ala Val Tyr Val Phe Met Gly Ala
 385 390 395 400
 Gly Asp Ile Gln Thr Tyr Glu Tyr Ser Phe Glu Arg Leu Leu Ser Asn
 405 410 415
 Leu Thr Ser Asn Val Gln
 420

(2) INFORMATION FOR SEQ ID NO: 117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3121 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

TTTAAACCCA ACTGTTGGTA CTTTCCTTTT TACTGCAGGA TTGACCTTGT TAGTTTTATT

GGTTTCTAAA AGGGAAAAATG GAAAGAAACG ACTTGTTCAT TTCTGCTGT TGACTAGCAT	120
GGGAGTTCAA TTGTTGCCGG CCACTGCTTT TGGGTTGACC AGCCAGATTT TATCTGCCTA	180
TAATAGTCAG CTTTCTATCG GAGTCGGGA ACATTTACCA GAGCCTCTGA AAATCGAAGG	240
TTATCAATAT ATTGGTTATA TCAAACTAA GAAACAGGAT AATACAGAGC TTTCAGGAC	300
AGTTGATGGG AAATACTCTG CTCAAAGAGA TAGTCAACCA AACTCTACAA AAACATCAGA	360
TGTAGTTCAT TCAGCTGATT TAGAATGGAA CCAAGGACAG GGAAGGTTA GTTTACAAGG	420
TGAAGCATCA GGGGATGATG GACTTTTCAGA AAAATCTTCT ATAGCAGCAG ACAATCTATC	480
TTCTAATGAT TCATTTCGCA GTCAAGTTGA GCAGAATCCG GATCACAAAG GAGAATCTGT	540
AGTTCGACCA ACAGTGCCAG AACAAAGAAA TCCTGTGTCT GCTACAACGG TGCAGAGTGC	600
GGAAGAGGAA GTATTGGCGA CGACAATGA TCGACCAGAG TATAAACTTC CATTGGAAAC	660
CAAAGGCACG CAAGAACCCG GTCATGAGGG TGAAGCCGCA GTCCGTGAAG ACTTACCAGT	720
CTACACTAAG CCACTAGAAA CCAAAGGTAC ACAAGGACCC GGACATGAAG GTGAAGCTGC	780
AGTTCGCGAG GAAGAACCAG CTTACACAGA ACCGTTAGCA ACGAAAGSCA CGCAAGAGCC	840
AGGTGATGAG GGCAAAGCTA CAGTCCGCGA AGAGACTCTA GAGTACACGG AACCGGTAGC	900
GACAAAAGGC ACACAAGAAC CCGAACATGA GGGCGAaCGG sCAGTAGAAG AAGAACTTCC	960
GGCTTTAGAG GTCACACAC GAAATAGAAC GGAATCCAG AATATTCCCTT ATACAACAGA	1020
AGAAATTGAG GATCCAACAC TTCTGAAAAA TCGTCGTAAG ATTGAACGAC AAGGGCAAGC	1080
AGGGACACGT ACAATTCAAT ATGAAGACTA CATCGTAAAT GGTAATGTCG TAGAAACTAA	1140
AGAAGTGTC CGAACTGAAG TAGCTCCGGT CAACGAAGTC GTTAAAGTAG GAACACTTGT	1200
GAAAGTTAAA CCTACAGTAG AAATTACAAA CTTAACAAAA GTTGAGAACA AAAAATCTAT	1260
AACGTGAAGT TATACTTAA TAGACACTAC CTCAGCATAT GTTTCTGCAA AAACGCAAGT	1320
TTTCCATGGA GACAAGCTAG TTAAGAGAGT GGATATAGAA AATCCTGCCA AAGAGCAAGT	1380
AATATCAGST TTAGATTACT ACACACCGTA TACAGTTAAA ACACACCTAA CTTATAATTT	1440
GGGTGAAAAA AATGAGGAAA ATACTGAAAC ATCAACTCAA GATTTCCTAA TAGAGTATAA	1500
GAAATAGAG ATTAAGATA TTGATTCAGT AGAATTATAC GGTAAAGAAA ATGATCGTTA	1560
TCGTAGATAT TTAAGCTTAA GTGAAGCGCC GACTGATACG GCTAAATACT TTGTAAAAGT	1620
GAAATCAGAT CGCTTCAAAG AAATGTACCT ACCTGTAAAA TCTATTACAG AAAATACGGA	1680
TGGAACGTAT AAGTGACGG TAGCCGTTGA TCAACTTTGC GAAGAAGGTA CAGACGGTTA	1740
CAAAGATGAT TACACATTTA CTGTAGCTAA ATCTAAAGCA GAGCAACCAG GAGTTTACAC	1800
ATCCTTTAAA CAGCTGGTAA CAGCCATGCA AAGCAATCTG TCTGGTGTCT ATACATTGGC	1860
TTCAGATATG ACCGCAGATG AGGTGAGCTT AGGCGATAAG CAGACAAGTT ATCTCACAGG	1920

TGCATTTACA GGGAGCTTGA TCGGTTCTGA TGGAACAAAA TCGTATGCCA TTTATGATTT 1980
 GAAGAAACCA TTATTGATA CATTAAATGG TGCTACAGTT AGAGATTGG ATATTAAAC 2040
 TGTTCCTGCT GATAGTAAAG AAAATGTCGC AGCGCTGGCG AAGGCAGCGA ATAGCGCGAA 2100
 TATTAATAAT GTTGCACTAG AAGGAAAAAT CTCAGGTGCG AATCTGTGTG CGGGATTAGT 2160
 AGCGAGCGCA ACAAATACAG TGATAGAAAA CAGCTCGTTT ACAGGGAAC TTATCGCAAA 2220
 TCACCAAGCAG AGTAATAAAA ATGATACTGG AGGAATAGTA GGTAAATATA CAGGAAATAG 2280
 TTCGAGAGTT AATAAGTTA GGGTAGATGC CTTAATCTCT ACTAATGCAC GCAATAATAA 2340
 CCAACAGCT GGAGGGATAG TAGGTAGATT AGAAAATGGT GCATTGATAT CTAATTCGGT 2400
 TGCTACTGGA GAAATACGAA ATGGTCAAGG ATATTCTAGA GTCGGAGGAA TAGTAGGATC 2460
 TACGTGGCAA AACGGTCGAG TAAATAATGT TGTGAGTAAC GTAGATGTTG GAGATGGTTA 2520
 TGTATTACCC GGTGATCAAT ACGCAGCAGC AGATGTGAAA AATGCAAGTA CATCAGTTGA 2580
 TAATAGAAAA GCAGACAGAT TCGCTACAAA ATTATCAAAA GACCAAAATAG ACGCGAAAGT 2640
 TGCTGATTAT GGAATCACAG TAACTCTTGA TGATACTGGG CAAGATTTAA AACGTAATCT 2700
 AAGAGAAGTT GATTATACAA GACTAAATAA AGCAGAAGCT GAAAGAAAAG TAGCTTATAG 2760
 CAACATAGAA AACTGATGTC CATTCTACAA TAAGACCTA GTAGTTCCT ATGTTAACAA 2820
 AGTAGCGACA ACAGATAAAC TTTACACTAC AGAATTGTTA GATGTTGTGC CGATGAAAGA 2880
 TGATGAAGTA GTAACGATA TTAATAATAA GAAAAATTCA ATAAATAAAG TTATGTTACA 2940
 TTTCAAAGAT AATACAGTAG AATACCTAGA TGTAACTTCA AAAGAAAAC TCATAAACAG 3000
 TCAAGTAATC GAATACAATG TTACAGGAAA AGAATATATA TTCACACCAG AAGCATTGTT 3060
 TTCAGACTAT ACAGCGATAA CGAATAACGT ACTAAGCGAC TTGCAAAATG TAACACTTAA 3120
 C 3121

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1040 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

Phe Asn Pro Thr Val Gly Thr Phe Leu Phe Thr Ala Gly Leu Ser Leu
 1 5 10 15
 Leu Val Leu Leu Val Ser Lys Arg Glu Asn Gly Lys Lys Arg Leu Val
 20 25 30
 His Phe Leu Leu Leu Thr Ser Met Gly Val Gln Leu Leu Pro Ala Ser
 35 40 45

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Ala Phe Gly Leu Thr Ser Gln Ile Leu Ser Ala Tyr Asn Ser Gln Leu
 50 55 60
 Ser Ile Gly Val Gly Glu His Leu Pro Glu Pro Leu Lys Ile Glu Gly
 65 70 75 80
 Tyr Gln Tyr Ile Gly Tyr Ile Lys Thr Lys Lys Gln Asp Asn Thr Glu
 85 90 95
 Leu Ser Arg Thr Val Asp Gly Lys Tyr Ser Ala Gln Arg Asp Ser Gln
 100 105 110
 Pro Asn Ser Thr Lys Thr Ser Asp Val Val His Ser Ala Asp Leu Glu
 115 120 125
 Trp Asn Gln Gly Gln Gly Lys Val Ser Leu Gln Gly Glu Ala Ser Gly
 130 135 140
 Asp Asp Gly Leu Ser Glu Lys Ser Ser Ile Ala Ala Asp Asn Leu Ser
 145 150 155 160
 Ser Asn Asp Ser Phe Ala Ser Gln Val Glu Gln Asn Pro Asp His Lys
 165 170 175
 Gly Glu Ser Val Val Arg Pro Thr Val Pro Glu Gln Gly Asn Pro Val
 180 185 190
 Ser Ala Thr Thr Val Gln Ser Ala Glu Glu Glu Val Leu Ala Thr Thr
 195 200 205
 Asn Asp Arg Pro Glu Tyr Lys Leu Pro Leu Glu Thr Lys Gly Thr Gln
 210 215 220
 Glu Pro Gly His Glu Gly Glu Ala Ala Val Arg Glu Asp Leu Pro Val
 225 230 235 240
 Tyr Thr Lys Pro Leu Glu Thr Lys Gly Thr Gln Gly Pro Gly His Glu
 245 250 255
 Gly Glu Ala Ala Val Arg Glu Glu Glu Pro Ala Tyr Thr Glu Pro Leu
 260 265 270
 Ala Thr Lys Gly Thr Gln Glu Pro Gly His Glu Gly Lys Ala Thr Val
 275 280 285
 Arg Glu Glu Thr Leu Glu Tyr Thr Glu Pro Val Ala Thr Lys Gly Thr
 290 295 300
 Gln Glu Pro Glu His Glu Gly Glu Arg Xaa Val Glu Glu Glu Leu Pro
 305 310 315 320
 Ala Leu Glu Val Thr Thr Arg Asn Arg Thr Glu Ile Gln Asn Ile Pro
 325 330 335
 Tyr Thr Thr Glu Glu Ile Gln Asp Pro Thr Leu Leu Lys Asn Arg Arg
 340 345 350
 Lys Ile Glu Arg Gln Gly Gln Ala Gly Thr Arg Thr Ile Gln Tyr Glu
 355 360 365
 Asp Tyr Ile Val Asn Gly Asn Val Val Glu Thr Lys Glu Val Ser Arg
 370 375 380

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Thr Glu Val Ala Pro Val Asn Glu Val Val Lys Val Gly Thr Leu Val
 385 390 395 400
 Lys Val Lys Pro Thr Val Glu Ile Thr Asn Leu Thr Lys Val Glu Asn
 405 410 415
 Lys Lys Ser Ile Thr Val Ser Tyr Asn Leu Ile Asp Thr Thr Ser Ala
 420 425 430
 Tyr Val Ser Ala Lys Thr Gln Val Phe His Gly Asp Lys Leu Val Lys
 435 440 445
 Glu Val Asp Ile Glu Asn Pro Ala Lys Glu Gln Val Ile Ser Gly Leu
 450 455 460
 Asp Tyr Tyr Thr Pro Tyr Thr Val Lys Thr His Leu Thr Tyr Asn Leu
 465 470 475 480
 Gly Glu Asn Asn Glu Glu Asn Thr Glu Thr Ser Thr Gln Asp Phe Gln
 485 490 495
 Leu Glu Tyr Lys Lys Ile Glu Ile Lys Asp Ile Asp Ser Val Glu Leu
 500 505 510
 Tyr Gly Lys Glu Asn Asp Arg Tyr Arg Arg Tyr Leu Ser Leu Ser Glu
 515 520 525
 Ala Pro Thr Asp Thr Ala Lys Tyr Phe Val Lys Val Lys Ser Asp Arg
 530 535 540
 Phe Lys Glu Met Tyr Leu Pro Val Lys Ser Ile Thr Glu Asn Thr Asp
 545 550 555 560
 Gly Thr Tyr Lys Val Thr Val Ala Val Asp Gln Leu Val Glu Glu Gly
 565 570 575
 Thr Asp Gly Tyr Lys Asp Asp Tyr Thr Phe Thr Val Ala Lys Ser Lys
 580 585 590
 Ala Glu Gln Pro Gly Val Tyr Thr Ser Phe Lys Gln Leu Val Thr Ala
 595 600 605
 Met Gln Ser Asn Leu Ser Gly Val Tyr Thr Leu Ala Ser Asp Met Thr
 610 615 620
 Ala Asp Glu Val Ser Leu Gly Asp Lys Gln Thr Ser Tyr Leu Thr Gly
 625 630 635 640
 Ala Phe Thr Gly Ser Leu Ile Gly Ser Asp Gly Thr Lys Ser Tyr Ala
 645 650 655
 Ile Tyr Asp Leu Lys Lys Pro Leu Phe Asp Thr Leu Asn Gly Ala Thr
 660 665 670
 Val Arg Asp Leu Asp Ile Lys Thr Val Ser Ala Asp Ser Lys Glu Asn
 675 680 685
 Val Ala Ala Leu Ala Lys Ala Ala Asn Ser Ala Asn Ile Asn Asn Val
 690 695 700
 Ala Val Glu Gly Lys Ile Ser Gly Ala Lys Ser Val Ala Gly Leu Val
 705 710 715 720

Ala Ser Ala Thr Asn Thr Val Ile Glu Asn Ser Ser Phe Thr Gly Lys
725 730 735

Leu Ile Ala Asn His Gln Asp Ser Asn Lys Asn Asp Thr Gly Gly Ile
740 745 750

Val Gly Asn Ile Thr Gly Asn Ser Ser Arg Val Asn Lys Val Arg Val
755 760 765

Asp Ala Leu Ile Ser Thr Asn Ala Arg Asn Asn Asn Gln Thr Ala Gly
770 775 780

Gly Ile Val Gly Arg Leu Glu Asn Gly Ala Leu Ile Ser Asn Ser Val
785 790 795 800

Ala Thr Gly Glu Ile Arg Asn Gly Gln Gly Tyr Ser Arg Val Gly Gly
805 810 815

Ile Val Gly Ser Thr Trp Gln Asn Gly Arg Val Asn Asn Val Val Ser
820 825 830

Asn Val Asp Val Gly Asp Gly Tyr Val Ile Thr Gly Asp Gln Tyr Ala
835 840 845

Ala Ala Asp Val Lys Asn Ala Ser Thr Ser Val Asp Asn Arg Lys Ala
850 855 860

Asp Arg Phe Ala Thr Lys Leu Ser Lys Asp Gln Ile Asp Ala Lys Val
865 870 875 880

Ala Asp Tyr Gly Ile Thr Val Thr Leu Asp Asp Thr Gly Gln Asp Leu
885 890 895

Lys Arg Asn Leu Arg Glu Val Asp Tyr Thr Arg Leu Asn Lys Ala Glu
900 905 910

Ala Glu Arg Lys Val Ala Tyr Ser Asn Ile Glu Lys Leu Met Pro Phe
915 920 925

Tyr Asn Lys Asp Leu Val Val His Tyr Gly Asn Lys Val Ala Thr Thr
930 935 940

Asp Lys Leu Tyr Thr Thr Glu Leu Leu Asp Val Val Pro Met Lys Asp
945 950 955 960

Asp Glu Val Val Thr Asp Ile Asn Asn Lys Lys Asn Ser Ile Asn Lys
965 970 975

Val Met Leu His Phe Lys Asp Asn Thr Val Glu Tyr Leu Asp Val Thr
980 985 990

Phe Lys Glu Asn Phe Ile Asn Ser Gln Val Ile Glu Tyr Asn Val Thr
995 1000 1005

Gly Lys Glu Tyr Ile Phe Thr Pro Glu Ala Phe Val Ser Asp Tyr Thr
1010 1015 1020

Ala Ile Thr Asn Asn Val Leu Ser Asp Leu Gln Asn Val Thr Leu Asn
1025 1030 1035 1040

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1567 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

TTTTAACCCA ACTGTTGGTA CTTTCCTTTT TACTGCAGGA TTGAGCTTGT TAGTTTITATT	60
GGTTTCTAAA AGGGAAATG GAAAGAAACG ACTTGTTTCAT TTTCTGCTGT TGACTAGCAT	120
GGGAGTTCAA TTGTTGCCGG CCAGTGCTTT TGGGTTGACC AGCCAGATTT TATCTGCCTA	180
TAATAGTCAG CTTTCTATCG GAGTCGGGGA ACATTTACCA GAGCCTCTGA AAATCGAAGG	240
TTATCAATAT ATTGGTTATA TCAAAACTAA GAAACAGGAT AATACAGAGC TTTCAGGAC	300
AGTTGATGGG AAATACTCTG CTCAAAGAGA TAGTCAACCA AACTCTACAA AAACATCAGA	360
TGTAGTTTCAT TCAGCTGATT TAGAATGGAA CCAAGGACAG GGAAGGTTA GTTTACAAGG	420
TGAAGCATCA GGGGATGATG GACTTTCAGA AAAATCTTCT ATAGCAGCAG ACAATCTATC	480
TTCTAATGAT TCATTCGCAA GTCAAGTTGA GCAGAATCCG GATCACAAAG GAGAATCTGT	540
AGTTCGACCA ACAGTGCCAG AACAAAGAAA TCCTGTGTCT GCTACAACGG TGCAGAGTGC	600
GGAAGAGGAA GTATTGGCGA CGACAAATGA TCGACCAGAG TATAACTTC CATTGGAAC	660
CAAAGGCACG CAAGAACCCG GTCATGAGGG TGAAGCCGCA GTCCGTGAAG ACTTACCAGT	720
CTACACTAAG CCACTAGAAA CCAAAGGTAC ACAAGGACCC GGACATGAAG GTGAAGTGC	780
AGTTCGCGAG GAAGAACCAG CTTACACAGA ACCGTTAGCA ACGAAAGGCA CGCAAGAGCC	840
AGGTCATGAG GSCAAAGCTA CAGTCCGCGA AGAGACTCTA GAGTACACGG AACCAGTAGC	900
GACAAAAGGC ACACAAGAAC CCGAACATGA GGGCGAaCGG sCAGTAGAAG AAGAATCTCC	960
GGCTTTAGAG GTCACATAC GAAATAGAAC GGAAATCCAG AATATTCCCTT ATACAACAGA	1020
AGAAATTCAG GATCCAACAC TTCTGAAAAA TCGTCGTAAG ATTGAACGAC AAGGGCAAGC	1080
AGGGACACGT ACAATTCAT ATGAAGACTA CATCGTAAAT GGTAATGTCG TAGAAACTAA	1140
AGAAGTGTCG CGAACTGAAG TAGCTCCGGT CAACGAAGTC GTTAAAGTAG GAACACTTGT	1200
GAAAGTTAAA CCTACAGTAG AAATTACAAA CTTAACAAAA GTTGAGAACA AAAAATCTAT	1260
AACGTGAAGT TATAACTTAA TAGACACTAC CTCAGCATAT GTTTCGCAA AAACGCAAGT	1320
TTTCCATGGA GACAAGCTAG TTAAAGAGGT GGATATAGAA AATCCTGCCA AAGAGCAAGT	1380
AATATCAGGT TTAGATTACT ACACACCGTA TACAGTTAAA ACACACCTAA CTTATAATTT	1440
GGGTGAAAT AATGAGGAAA ATACTGAAAC ATCAACTCAA GATTTCGAAT TAGAGTATAA	1500
GAAAAATAGAG ATTAAAGATA TTGATTCAGT AGAATTATAC GGTAAGGAAA ATGATCGTTA	1560
TCGTAGA	1567

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(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 522 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

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Phe Asn Pro Thr Val Gly Thr Phe Leu Phe Thr Ala Gly Leu Ser Leu
1          5          10          15
Leu Val Leu Leu Val Ser Lys Arg Glu Asn Gly Lys Lys Arg Leu Val
20          25          30
His Phe Leu Leu Leu Thr Ser Met Gly Val Gln Leu Leu Pro Ala Ser
35          40          45
Ala Phe Gly Leu Thr Ser Gln Ile Leu Ser Ala Tyr Asn Ser Gln Leu
50          55          60
Ser Ile Gly Val Gly Glu His Leu Pro Glu Pro Leu Lys Ile Glu Gly
65          70          75          80
Tyr Gln Tyr Ile Gly Tyr Ile Lys Thr Lys Lys Gln Asp Asn Thr Glu
85          90          95
Leu Ser Arg Thr Val Asp Gly Lys Tyr Ser Ala Gln Arg Asp Ser Gln
100         105         110
Pro Asn Ser Thr Lys Thr Ser Asp Val Val His Ser Ala Asp Leu Glu
115         120         125
Trp Asn Gln Gly Gln Gly Lys Val Ser Leu Gln Gly Glu Ala Ser Gly
130         135         140
Asp Asp Gly Leu Ser Glu Lys Ser Ser Ile Ala Ala Asp Asn Leu Ser
145         150         155         160
Ser Asn Asp Ser Phe Ala Ser Gln Val Glu Gln Asn Pro Asp His Lys
165         170         175
Gly Glu Ser Val Val Arg Pro Thr Val Pro Glu Gln Gly Asn Pro Val
180         185         190
Ser Ala Thr Thr Val Gln Ser Ala Glu Glu Glu Val Leu Ala Thr Thr
195         200         205
Asn Asp Arg Pro Glu Tyr Lys Leu Pro Leu Glu Thr Lys Gly Thr Gln
210         215         220
Glu Pro Gly His Glu Gly Glu Ala Ala Val Arg Glu Asp Leu Pro Val
225         230         235         240
Tyr Thr Lys Pro Leu Glu Thr Lys Gly Thr Gln Gly Pro Gly His Glu
245         250         255
Gly Glu Ala Ala Val Arg Glu Glu Glu Pro Ala Tyr Thr Glu Pro Leu

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260

265

270

Ala Thr Lys Gly Thr Gln Glu Pro Gly His Glu Gly Lys Ala Thr Val
 275 280 285

Arg Glu Glu Thr Leu Glu Tyr Thr Glu Pro Val Ala Thr Lys Gly Thr
 290 295 300

Gln Glu Pro Glu His Glu Gly Glu Arg Xaa Val Glu Glu Glu Leu Pro
 305 310 315 320

Ala Leu Glu Val Thr Thr Arg Asn Arg Thr Glu Ile Gln Asn Ile Pro
 325 330 335

Tyr Thr Thr Glu Glu Ile Gln Asp Pro Thr Leu Leu Lys Asn Arg Arg
 340 345 350

Lys Ile Glu Arg Gln Gly Gln Ala Gly Thr Arg Thr Ile Gln Tyr Glu
 355 360 365

Asp Tyr Ile Val Asn Gly Asn Val Val Glu Thr Lys Glu Val Ser Arg
 370 375 380

Thr Glu Val Ala Pro Val Asn Glu Val Val Lys Val Gly Thr Leu Val
 385 390 395 400

Lys Val Lys Pro Thr Val Glu Ile Thr Asn Leu Thr Lys Val Glu Asn
 405 410 415

Lys Lys Ser Ile Thr Val Ser Tyr Asn Leu Ile Asp Thr Thr Ser Ala
 420 425 430

Tyr Val Ser Ala Lys Thr Gln Val Phe His Gly Asp Lys Leu Val Lys
 435 440 445

Glu Val Asp Ile Glu Asn Pro Ala Lys Glu Gln Val Ile Ser Gly Leu
 450 455 460

Asp Tyr Tyr Thr Pro Tyr Thr Val Lys Thr His Leu Thr Tyr Asn Leu
 465 470 475 480

Gly Glu Asn Asn Glu Glu Asn Thr Glu Thr Ser Thr Gln Asp Phe Gln
 485 490 495

Leu Glu Tyr Lys Lys Ile Glu Ile Lys Asp Ile Asp Ser Val Glu Leu
 500 505 510

Tyr Gly Lys Glu Asn Asp Arg Tyr Arg Arg
 515 520

(2) INFORMATION FOR SEQ ID NO: 121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1561 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

TCGTAGATAT TTAAGTCTAA GTGAAGCGCC GACTGATACG GCTAAATACT TTGTAAAGT

GAAATCAGAT CGCTTCAAAG AAATGTACCT ACCTGTAAAA TCTATTACAG AAAATACGGA 120
 TGGAACGTAT AAAGTGACGG TAGCCGTTGA TCAACTTGTC GAAGAAGGTA CAGACGGTTA 180
 CAAAGATGAT TACACATTTA CTGTAGCTAA ATCTAAAGCA GAGCAACCAG GAGTTTACAC 240
 ATCCTTTAAA CAGCTGGTAA CAGCCATGCA AAGCAATCTG TCTGGTGTCT ATACATTGGC 300
 TTCAGATATG ACCGCAGATG AGGTGAGCTT AGGCATAAG CAGACAAGTT ATCTCACAGG 360
 TGCATTTACA GGGAGCTTGA TCGGTTCTGA TGGAACAAA TCGTATGCCA TTTATGATTT 420
 GAAGAAACCA TTATTTGATA CATTAAATGG TGCTACAGTT AGAGATTTGG ATATTAAAC 480
 TGTTTCTGCT GATAGTAAAG AAAATGTCGC AGCGCTGGCG AAGGCAGCGA ATAGCGCGAA 540
 TATTATAAT GTTGAGTAG AAGGAAAAAT CTCAGGTGCG AAATCTGTTG CGGGATTAGT 600
 AGCGAGCGCA ACAATACAG TGATAGAAAA CAGCTCGTTT ACAGGGAAAC TTATCGCAAA 660
 TCACCAGGAC AGTAATAAAA ATGATACTGG AGGAATAGTA GGAATATAA CAGGAAATAG 720
 TTCGAGAGTT AATAAAGTTA GGGTAGATGC CTTAATCTCT ACTAATGCAC GCAATAATAA 780
 CCAACACGCT GGAGGGATAG TAGGTAGATT AGAAAATGGT GCATTGATAT CTAATTCGGT 840
 TGCTACTGGA GAAATACGAA ATGGTCAAGG ATATTCTAGA GTCGGAGGAA TAGTAGGATC 900
 TACGTGGCAA AACGTCGAG TAAATAATGT TGTGAGTAAC GTAGATGTTG GAGATGGTTA 960
 TGTTATCACC GGTGATCAAT ACGCAGCAGC AGATGTGAAA AATGCAAGTA CATCAGTTGA 1020
 TAATAGAAAA GCAGACAGAT TCGCTACAAA ATTATCAAAA GACCAAAATAG ACGCGAAAGT 1080
 TGCTGATTAT GGAATCAGAG TAACTCTTGA TGATACTGGG CAAGATTIAA AACGTAATCT 1140
 AAGAGAAGTT GATTATACAA GACTAAATAA AGCAGAAGCT GAAAGAAAAG TAGCTTATAG 1200
 CAACATAGAA AACTGTATGC CATTCTACAA TAAAGACCTA GTAGTTCACT ATGTAACAA 1260
 AGTAGCGACA ACAGATAAAC TTTACACTAC AGAATTGTTA GATGTTGTGC CGATGAAGA 1320
 TGATGAAGTA GTAACGATA TTAATAATAA GAAAAATTCA ATAAATAAAG TTATGTTACA 1380
 TTTCAAAGAT AATACAGTAG AATACCTAGA TGTAACTTC AAAGAAAACT TCATAACAG 1440
 TCAAGTAATC GAATACAATG TTACAGGAAA AGAATATATA TTCACACCAG AAGCATTTGT 1500
 TTCAGACTAT ACAGCGATAA CGAATAACGT ACTAAGCGAC TTGCAAAATG TAACACTTAA 1560
 C

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 520 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

0975527.01220

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

Arg Arg Tyr Leu Ser Leu Ser Glu Ala Pro Thr Asp Thr Ala Lys Tyr
 1 5 10 15
 Phe Val Lys Val Lys Ser Asp Arg Phe Lys Glu Met Tyr Leu Pro Val
 20 25 30
 Lys Ser Ile Thr Glu Asn Thr Asp Gly Thr Tyr Lys Val Thr Val Ala
 35 40 45
 Val Asp Gln Leu Val Glu Glu Gly Thr Asp Gly Tyr Lys Asp Asp Tyr
 50 55 60
 Thr Phe Thr Val Ala Lys Ser Lys Ala Glu Gln Pro Gly Val Tyr Thr
 65 70 75 80
 Ser Phe Lys Gln Leu Val Thr Ala Met Gln Ser Asn Leu Ser Gly Val
 85 90 95
 Tyr Thr Leu Ala Ser Asp Met Thr Ala Asp Glu Val Ser Leu Gly Asp
 100 105 110
 Lys Gln Thr Ser Tyr Leu Thr Gly Ala Phe Thr Gly Ser Leu Ile Gly
 115 120 125
 Ser Asp Gly Thr Lys Ser Tyr Ala Ile Tyr Asp Leu Lys Lys Pro Leu
 130 135 140
 Phe Asp Thr Leu Asn Gly Ala Thr Val Arg Asp Leu Asp Ile Lys Thr
 145 150 155 160
 Val Ser Ala Asp Ser Lys Glu Asn Val Ala Ala Leu Ala Lys Ala Ala
 165 170 175
 Asn Ser Ala Asn Ile Asn Asn Val Ala Val Glu Gly Lys Ile Ser Gly
 180 185 190
 Ala Lys Ser Val Ala Gly Leu Val Ala Ser Ala Thr Asn Thr Val Ile
 195 200 205
 Glu Asn Ser Ser Phe Thr Gly Lys Leu Ile Ala Asn His Gln Asp Ser
 210 215 220
 Asn Lys Asn Asp Thr Gly Gly Ile Val Gly Asn Ile Thr Gly Asn Ser
 225 230 235 240
 Ser Arg Val Asn Lys Val Arg Val Asp Ala Leu Ile Ser Thr Asn Ala
 245 250 255
 Arg Asn Asn Asn Gln Thr Ala Gly Gly Ile Val Gly Arg Leu Glu Asn
 260 265 270
 Gly Ala Leu Ile Ser Asn Ser Val Ala Thr Gly Glu Ile Arg Asn Gly
 275 280 285
 Gln Gly Tyr Ser Arg Val Gly Gly Ile Val Gly Ser Thr Trp Gln Asn
 290 295 300
 Gly Arg Val Asn Asn Val Val Ser Asn Val Asp Val Gly Asp Gly Tyr
 305 310 315 320

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Val Ile Thr Gly Asp Gln Tyr Ala Ala Ala Asp Val Lys Asn Ala Ser
 325 330 335

Thr Ser Val Asp Asn Arg Lys Ala Asp Arg Phe Ala Thr Lys Leu Ser
 340 345 350

Lys Asp Gln Ile Asp Ala Lys Val Ala Asp Tyr Gly Ile Thr Val Thr
 355 360 365

Leu Asp Asp Thr Gly Gln Asp Leu Lys Arg Asn Leu Arg Glu Val Asp
 370 375 380

Tyr Thr Arg Leu Asn Lys Ala Glu Ala Glu Arg Lys Val Ala Tyr Ser
 385 390 395 400

Asn Ile Glu Lys Leu Met Pro Phe Tyr Asn Lys Asp Leu Val Val His
 405 410 415

Tyr Gly Asn Lys Val Ala Thr Thr Asp Lys Leu Tyr Thr Thr Glu Leu
 420 425 430

Leu Asp Val Val Pro Met Lys Asp Asp Glu Val Val Thr Asp Ile Asn
 435 440 445

Asn Lys Lys Asn Ser Ile Asn Lys Val Met Leu His Phe Lys Asp Asn
 450 455 460

Thr Val Glu Tyr Leu Asp Val Thr Phe Lys Glu Asn Phe Ile Asn Ser
 465 470 475 480

Gln Val Ile Glu Tyr Asn Val Thr Gly Lys Glu Tyr Ile Phe Thr Pro
 485 490 495

Glu Ala Phe Val Ser Asp Tyr Thr Ala Ile Thr Asn Asn Val Leu Ser
 500 505 510

Asp Leu Gln Asn Val Thr Leu Asn
 515 520

(2) INFORMATION FOR SEQ ID NO: 123:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 850 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

CTTTGTTT GAAGGAAGTA AGCGTGACA ATTTGCTGTA GAAGGAATCA ATCAACTTCG	60
TGAGCATGTA GACACTCTAT TGATTATCTC AAACAACAAT TTGCTTGAAA TTGTTGATAA	120
GAAACACCG CTTTTGGAGG CTCTTAGCGA AGCGGATAAC GTTCTTCGTC AAGGTGTTCA	180
AGGGATTACC GATTTGATTA CCAATCCAGG ATTGATTAAC CTTGACTTTG CCGATGTGAA	240
AACGGTAATG GCAACAAAG GGAATGCTCT TATGGGTATT GGTATCGGTA GTGAGAAGA	300
ACGTGTGGTA GAAGCGGCAC GTAAGGCAAT CTATTCACCA CTCTTGAAA CAACTATTGA	360

CGSTGCTGAG GATGTTATCG TCAACGTTAC TGGTGGTCTT GACTTAACCT TGATTGAGGC 420
 AGAAGAGGCT TCACAAATTG TGAACCAGGC AGCAGGTCAA GGAGTGAACA TCTGGCTCGG 480
 TACTTCAATT GATGAAAGTA TGCCTGATGA AATTCGTGTA ACAGTTGTTG CAACGGGTGT 540
 TCGTCAAGAC CGCGTAGAAA AGGTTGTGGC TCCACAAGCT AGATCTGCTA CTAACACCAG 600
 TGAGACAGTG AAACCAGCTC ATTCACATGG CTTTGATCGT CATTTTGATA TGGCAGAAAC 660
 AGTTGAATTG CCAAAACAAA ATCCACGTCG TTGGAACCA ACTCAGGCAT TGCTTTTGG 720
 TGATTGGGAT CTTCGCCGTG AATCGATTGT TCGTACAACA GATTCAGTCG TTTCTCCAGT 780
 CGAGCGCTTT GAAGCCCCAA TTTCACAAGA TGAAGATGAA TTGGATACAC CTCCATTTTT 840
 CAAAAATCGT 850

(2) INFORMATION FOR SEQ ID NO:124:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 283 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

Phe Gly Phe Glu Gly Ser Lys Arg Gly Gln Phe Ala Val Glu Gly Ile
 1 5 10 15
 Asn Gln Leu Arg Glu His Val Asp Thr Leu Leu Ile Ile Ser Asn Asn
 20 25 30
 Asn Leu Leu Glu Ile Val Asp Lys Lys Thr Pro Leu Leu Glu Ala Leu
 35 40 45
 Ser Glu Ala Asp Asn Val Leu Arg Gln Gly Val Gln Gly Ile Thr Asp
 50 55 60
 Leu Ile Thr Asn Pro Gly Leu Ile Asn Leu Asp Phe Ala Asp Val Lys
 65 70 75 80
 Thr Val Met Ala Asn Lys Gly Asn Ala Leu Met Gly Ile Gly Ile Gly
 85 90 95
 Ser Gly Glu Glu Arg Val Val Glu Ala Ala Arg Lys Ala Ile Tyr Ser
 100 105 110
 Pro Leu Leu Glu Thr Thr Ile Asp Gly Ala Glu Asp Val Ile Val Asn
 115 120 125
 Val Thr Gly Gly Leu Asp Leu Thr Leu Ile Glu Ala Glu Glu Ala Ser
 130 135 140
 Gln Ile Val Asn Gln Ala Ala Gly Gln Gly Val Asn Ile Trp Leu Gly
 145 150 155 160
 Thr Ser Ile Asp Gly Ser Met Arg Asp Glu Ile Arg Val Thr Val Val
 165 170 175

Ala Thr Gly Val Arg Gln Asp Arg Val Glu Lys Val Val Ala Pro Gln
 180 185 190

Ala Arg Ser Ala Thr Asn Tyr Arg Glu Thr Val Lys Pro Ala His Ser
 195 200 205

His Gly Phe Asp Arg His Phe Asp Met Ala Glu Thr Val Glu Leu Pro
 210 215 220

Lys Gln Asn Pro Arg Arg Leu Glu Pro Thr Gln Ala Ser Ala Phe Gly
 225 230 235 240

Asp Trp Asp Leu Arg Arg Glu Ser Ile Val Arg Thr Thr Asp Ser Val
 245 250 255

Val Ser Pro Val Glu Arg Phe Glu Ala Pro Ile Ser Gln Asp Glu Asp
 260 265 270

Glu Leu Asp Thr Pro Pro Phe Phe Lys Asn Arg
 275 280

(2) INFORMATION FOR SEQ ID NO: 125:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1051 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

CTACTACCTC TCGAGAGAAA GTGACCTAGA GGTGACCGTT TTGACCATG AGCAAAGTCA	60
AGCCACCAAG GCCGCAGCAG GAATTATCAG TCCTTGGTTT TCCAAACGCC GTAATAAAGC	120
CTGGTACAAG ATGGCGCGCT TGGGGGCTGA TTTTATGTG GATTATTAG CTGATTAGA	180
GAAATCAGGA CAAGAAATCG ACTTTTACCA GCGTTCGGGA GTCTTCTCT TGAAAAAGGA	240
TGAATCCAAT TTGAAGAAC TTTATCAACT GGCCCTCCAG CGCAGAGAAG AATCTCCCTT	300
GATAGGGCAA TTAGCCAATC TGAACCAAGC CTCAGCTAAT GAATTATTCC CTGGTTTGCA	360
GGGATTTGAC CGCCTGCTCT ATGCTTCTGG TGGAGCGAGA GTAGATGGCC AACTTTTAGT	420
GACTCGTTTG CTGGAAGTCA GTCATGTCAA GCTGGTCAAA GAAAAAGTGA CTCTGACACC	480
GTTAGCATCA GCTACCAGA TTGGTGAAGA GGAGTTTGG CAGGTTATTT TGGCGACGGG	540
AGCTTGTTGG TGGGACATGT TAGAGCCTTT AGGTTATGAA TGGATGTCC GTCCCTCAAAA	600
AGGACAAC TAAGATTATC AGCTTGCCCA AGACATGGA GATTACCTGT TGTGTCATGCC	660
AGAAGGGGGG TGGGATTTGA TTCCCTTTGC AGGTGGGAAA TTATCTTTAG GCGCTACCCA	720
CGAAAATGAC ATGGGATTGT ATTTGACGGT AGATGAAACC TTGCTCCAAC AAATGGAGGA	780
GGCCACCTTG ACTCACTATC TGATTTTGGC TGAAGCTACT TCAAAATCTG AGCGTGTGG	840
AATCCGTGCC TACACCAGTG ATTTCTCTCC TTCTTTGGG CAGGTGCCTG ACTTAACCTG	900

TGTCATGCA GCCAGTGGAC TAGGTTTCATC AGGCCTCACA ACTGGTCCTA TCATTGGTTA 960
 CCATCTAGCC CAACTGATCC AAGACAAGGA GTTGACCTTG GACCCTCTAA ATTACCCAAT 1020
 TGAATACTAT GTCAAACGAG TAAAAAGCGA A 1051

(2) INFORMATION FOR SEQ ID NO:126:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 350 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

Tyr Tyr Leu Ser Arg Glu Ser Asp Leu Glu Val Thr Val Phe Asp His
 1 5 10 15
 Glu Gln Gly Gln Ala Thr Lys Ala Ala Gly Ile Ile Ser Pro Trp
 20 25 30
 Phe Ser Lys Arg Arg Asn Lys Ala Trp Tyr Lys Met Ala Arg Leu Gly
 35 40 45
 Ala Asp Phe Tyr Val Asp Leu Leu Ala Asp Leu Glu Lys Ser Gly Gln
 50 55 60
 Glu Ile Asp Phe Tyr Gln Arg Ser Gly Val Phe Leu Leu Lys Lys Asp
 65 70 75 80
 Glu Ser Asn Leu Glu Glu Leu Tyr Gln Leu Ala Leu Gln Arg Arg Glu
 85 90 95
 Glu Ser Pro Leu Ile Gly Gln Leu Ala Ile Leu Asn Gln Ala Ser Ala
 100 105 110
 Asn Glu Leu Phe Pro Gly Leu Gln Gly Phe Asp Arg Leu Leu Tyr Ala
 115 120 125
 Ser Gly Gly Ala Arg Val Asp Gly Gln Leu Leu Val Thr Arg Leu Leu
 130 135 140
 Glu Val Ser His Val Lys Leu Val Lys Glu Lys Val Thr Leu Thr Pro
 145 150 155 160
 Leu Ala Ser Gly Tyr Gln Ile Gly Glu Glu Glu Phe Glu Gln Val Ile
 165 170 175
 Leu Ala Thr Gly Ala Trp Leu Gly Asp Met Leu Glu Pro Leu Gly Tyr
 180 185 190
 Glu Val Asp Val Arg Pro Gln Lys Gly Gln Leu Arg Asp Tyr Gln Leu
 195 200 205
 Ala Gln Asp Met Glu Asp Tyr Pro Val Val Met Pro Glu Gly Glu Trp
 210 215 220
 Asp Leu Ile Pro Phe Ala Gly Gly Lys Leu Ser Leu Gly Ala Thr His

(2) INFORMATION FOR SEO ID NO: 127:

(A) LENGTH: 352 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

TAAGGTCAAA AGTCAGACCG CTAAGAAAGT GCTAGAAAAAG ATTGGAGCTG ACTCGGTTAT	60
CTCGCCAGAG TATGAAATGG GGCAGTCTCT AGCACAGACC ATYCTTTTCC ATAATAGTGT	120
TGATGTCTTT CAGTTGGATA AAAATGTGTC TATCGTGGAG ATGAAAAATC CTCAGTCTTG	180
GGCAGGTCAA AGTCTGAGTA AATTAGACCT CCGTGGCAAA TACAATCTGA ATATTTTGGG	240
TTTCCGAGAG CAGGAAAAAT CCCCATGGA TGTGAATTG GGACCAGATG ACCTCTTGAA	300
AGCAGATACC TATATTTTGG CAGTCATCAA CAACCAAGTAT TTGGATACCC TA	352

(A) LENGTH: 117 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEO ID NO:128:

Lys Val Lys Ser Gln Thr Ala Lys Lys Val Leu Glu Lys Ile Gly Ala
1 5 10 15

```

Asp Ser Val Ile Ser Pro Glu Tyr Glu Met Gly Gln Ser Leu Ala Gln
    20          25          30

Thr Ile Leu Phe His Asn Ser Val Asp Val Phe Gln Leu Asp Lys Asn
    35          40          45

Val Ser Ile Val Glu Met Lys Ile Pro Gln Ser Trp Ala Gly Gln Ser
    50          55          60

Leu Ser Lys Leu Asp Leu Arg Gly Lys Tyr Asn Leu Asn Ile Leu Gly
    65          70          75          80

Phe Arg Glu Gln Glu Asn Ser Pro Leu Asp Val Glu Phe Gly Pro Asp
    85          90          95

Asp Leu Leu Lys Ala Asp Thr Tyr Ile Leu Ala Val Ile Asn Asn Gln
    100          105          110

Tyr Leu Asp Thr Leu
    115

```

(2) INFORMATION FOR SEQ ID NO: 129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 247 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

```

TGACGGGTCT CAGGATCAGA CTCAGGAAAT CGCTGAGTGT TTAGCTAGCA AGTATCCTAA      60
TATCGTTAGA GCCATCTATC AGGAAAATAA ATGCCATGSC GGTGCGGTCA ATCGTGGCTT      120
GGTAGAGGCT TCTGGGCGCT ATTTTAAAGT AGTTGACAGT GATGACTGGG TGGATCCTCG      180
TGCCTACTTG AAAATCTTGT AAACCTGCAG GAACCTGAGA GCAAAGGTCA AGAGGTGGAT      240
GTCTTTG                                     247

```

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

```

Asp Gly Ser Gln Asp Gln Thr Gln Glu Ile Ala Glu Cys Leu Ala Ser
  1          5          10          15

Lys Tyr Pro Asn Ile Val Arg Ala Ile Tyr Gln Glu Asn Lys Cys His
  20          25          30

Gly Gly Ala Val Asn Arg Gly Leu Val Glu Ala Ser Gly Arg Tyr Phe

```

35

40

45

Lys Val Val Asp Ser Asp Asp Trp Val Asp Pro Arg Ala Tyr Leu Lys
50 55 60

Ile Leu Glu Thr Cys Arg Asn Leu Arg Ala Lys Val Lys Arg Trp Met
65 70 75 80

Ser Leu

(2) INFORMATION FOR SEQ ID NO: 131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1744 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

TAGAGGCTTT GCCAAATGGT GGAAGGGCA CGAGCGTCGA AAAGAGGAAC GCTTTGTCAA	60
ACAAGAAGAA AAAGCTCGCC AAAAGGCTGA GAAAGAGGCT AGATTAGAAC AAGAAGAGAC	120
TGAAAAAGCC TTA CTCTGATT TGCCTCCTGT TGATATGGAA ACGGGTGAAA TTCTGACAGA	180
GGAAGCTGTT CAAAATCTTC CACCTATTCC AGAAGAAAAA TGGGTGGAAC CAGAAATCAT	240
CCTGCCTCAA GCTGAACTTA AATTCCCTGA ACAGGAAGAT GACTCAGATG ACGAAGATGT	300
TCAGGTCGAT TTTCAGCCA AAGAAGCCCT TGAATACAAA CTTCACAGCT TACAACCTCTT	360
TGCACCAGAT AAACCAAAG ATCAGTCTAA AGAGAAGAAA ATTGTCAGAG AAAATATCAA	420
AATCTTAGAA GCAACCTTTG CTAGCTTTGG TATTAAGGTA ACAGTTGAAC GGGCCGAAAT	480
TGGGCCATCA GTGACCAAGT ATGAAGTCAA GCCGGCTGTT GGTGTAAGGG TCAACCGCAT	540
TTCCAATCTA TCAGATGACC TCGCTCTAGC CTTGGCTGCC AAAGATGTCC GGATTGAAGC	600
ACCAATCCCT GGGAAATCCC TAATCGGAAT TGAAGTGGCC AACTCCGATA TTGCCACTGT	660
ATCTTTCCGA GAACTATGGG AACAATCGCA AACGAAAGCA GAAAATTTCT TGGAAATTC	720
TTTAGGGAAG GCTGTTAATG GAACCGAAG AGCTTTTGAC CTTTCTAAAA TGCCCCACTT	780
GCTAGTTGCA GGTTCACGCG GTTCAGGGAA GTCAGTAGCA GTTACCGCA TTAATTGCTAG	840
CATTCTCATG AAGGCGAGAC CAGATCAAGT TAAATTATG ATGTCGATC CCAAGATGGT	900
TGAGTTATCT GTTTACAATG ATATTCCCCA CCTCTTGATT CCAGTCGTGA CCAATCCAGG	960
CAAGGCCAGC AAGGCTCTGC AAAAGGTTGT GGATGAAGAT GAAAACCGTT ATGAACCTTT	1020
TGCCAAGGCT GGAGTTCCGA ATATTGCAGG TTTTAATGCC AAGGTAGAAG AGTTCAATT	1080
CCAGTCTGAG TACAAGCAAA TTCCGCTACC ATTCATTGTC GTGATTGTGG ATGAGTTGGC	1140
TGACCTCATG ATGGTGGCCA GCAAGGAAGT GGAAGATGTC ATCATCCGTC TTGGGCAGAA	1200

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GGCGCGTGCT GCAGGTATCC ACATGATTCT TGCAACTCAG CGTCCATCTG TTGATGTCAT 1260
 CTCTGGTTTG ATTAAGSCCA ATGTTCCATC TCGTGTAGCA TTTGCGSTTT CATCAGGAAC 1320
 AGACTCCCGT ACGATTTTGG ATGAAAATGG AGCAGAAAAA CTTCTTGGTC GAGGAGACAT 1380
 GCTCTTTAAA CCGATTGATG AAAATCATCC AGTTCGTCTC CAAGGCTCCT TTAATCTCGGA 1440
 TGACGATGTT GAGCGCATTG TGAAC TTCAT CAAGACTCAG GCAGATGCAG ACTACGATGA 1500
 GAGTTTTGAT CCAGGTGAGG TTTCTGAAAA TGAAGGAGAA TTTTCGGATG GAGATGCTGG 1560
 TGGTGATCCG CTTTGTGAAG AAGCTAAGTC TTTGGTTATC GAAACACAGA AAGCCAGTGC 1620
 GTCTATGATT CAGCGTCGTT TATCAGTTGG ATTTAACCCT GCGACCCGTC TCATGGAAGA 1680
 ACTGGAGATA GCAGGTGTCA TCGGTCCAGC TGAAGGTACC AAACCTCGAA AAGTGTTACA 1740
 ACAA 1744

(2) INFORMATION FOR SEQ ID NO:132:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 581 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

Arg Gly Phe Ala Lys Trp Trp Glu Gly His Glu Arg Arg Lys Glu Glu
 1 5 10 15
 Arg Phe Val Lys Gln Glu Glu Lys Ala Arg Gln Lys Ala Glu Lys Glu
 20 25 30
 Ala Arg Leu Glu Gln Glu Glu Thr Glu Lys Ala Leu Leu Asp Leu Pro
 35 40 45
 Pro Val Asp Met Glu Thr Gly Glu Ile Leu Thr Glu Glu Ala Val Gln
 50 55 60
 Asn Leu Pro Pro Ile Pro Glu Glu Lys Trp Val Glu Pro Glu Ile Ile
 65 70 75 80
 Leu Pro Gln Ala Glu Leu Lys Phe Pro Glu Gln Glu Asp Asp Ser Asp
 85 90 95
 Asp Glu Asp Val Gln Val Asp Phe Ser Ala Lys Glu Ala Leu Glu Tyr
 100 105 110
 Lys Leu Pro Ser Leu Gln Leu Phe Ala Pro Asp Lys Pro Lys Asp Gln
 115 120 125
 Ser Lys Glu Lys Lys Ile Val Arg Glu Asn Ile Lys Ile Leu Glu Ala
 130 135 140
 Thr Phe Ala Ser Phe Gly Ile Lys Val Thr Val Glu Arg Ala Glu Ile
 145 150 155 160

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Gly Pro Ser Val Thr Lys Tyr Glu Val Lys Pro Ala Val Gly Val Arg
 165 170 175
 Val Asn Arg Ile Ser Asn Leu Ser Asp Asp Leu Ala Leu Ala Leu Ala
 180 185 190
 Ala Lys Asp Val Arg Ile Glu Ala Pro Ile Pro Gly Lys Ser Leu Ile
 195 200 205
 Gly Ile Glu Val Pro Asn Ser Asp Ile Ala Thr Val Ser Phe Arg Glu
 210 215 220
 Leu Trp Glu Gln Ser Gln Thr Lys Ala Glu Asn Phe Leu Glu Ile Pro
 225 230 235 240
 Leu Gly Lys Ala Val Asn Gly Thr Ala Arg Ala Phe Asp Leu Ser Lys
 245 250 255
 Met Pro His Leu Leu Val Ala Gly Ser Thr Gly Ser Gly Lys Ser Val
 260 265 270
 Ala Val Asn Gly Ile Ile Ala Ser Ile Leu Met Lys Ala Arg Pro Asp
 275 280 285
 Gln Val Lys Phe Met Met Val Asp Pro Lys Met Val Glu Leu Ser Val
 290 295 300
 Tyr Asn Asp Ile Pro His Leu Leu Ile Pro Val Val Thr Asn Pro Arg
 305 310 315 320
 Lys Ala Ser Lys Ala Leu Gln Lys Val Val Asp Glu Met Glu Asn Arg
 325 330 335
 Tyr Glu Leu Phe Ala Lys Val Gly Val Arg Asn Ile Ala Gly Phe Asn
 340 345 350
 Ala Lys Val Glu Glu Phe Asn Ser Gln Ser Glu Tyr Lys Gln Ile Pro
 355 360 365
 Leu Pro Phe Ile Val Val Ile Val Asp Glu Leu Ala Asp Leu Met Met
 370 375 380
 Val Ala Ser Lys Glu Val Glu Asp Ala Ile Ile Arg Leu Gly Gln Lys
 385 390 395 400
 Ala Arg Ala Ala Gly Ile His Met Ile Leu Ala Thr Gln Arg Pro Ser
 405 410 415
 Val Asp Val Ile Ser Gly Leu Ile Lys Ala Asn Val Pro Ser Arg Val
 420 425 430
 Ala Phe Ala Val Ser Ser Gly Thr Asp Ser Arg Thr Ile Leu Asp Glu
 435 440 445
 Asn Gly Ala Glu Lys Leu Leu Gly Arg Gly Asp Met Leu Phe Lys Pro
 450 455 460
 Ile Asp Glu Asn His Pro Val Arg Leu Gln Gly Ser Phe Ile Ser Asp
 465 470 475 480
 Asp Asp Val Glu Arg Ile Val Asn Phe Ile Lys Thr Gln Ala Asp Ala
 485 490 495

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Asp Tyr Asp Glu Ser Phe Asp Pro Gly Glu Val Ser Glu Asn Glu Gly
 500 505 510
 Glu Phe Ser Asp Gly Asp Ala Gly Gly Asp Pro Leu Phe Glu Glu Ala
 515 520 525
 Lys Ser Leu Val Ile Glu Thr Gln Lys Ala Ser Ala Ser Met Ile Gln
 530 535 540
 Arg Arg Leu Ser Val Gly Phe Asn Arg Ala Thr Arg Leu Met Glu Glu
 545 550 555 560
 Leu Glu Ile Ala Gly Val Ile Gly Pro Ala Glu Gly Thr Lys Pro Arg
 565 570 575
 Lys Val Leu Gln Gln
 580

(2) INFORMATION FOR SEQ ID NO: 133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:

TCAAAAAGAG AAGGAAACT TGGTTATTGC TGGGAAAATA GGTCCAGAAC CAGAAATTTT	60
GGCCAATATG TATAAGTTGC TGATTGAAGA AAATACCAGC ATGACTGCGA CTGTAAACC	120
GAATTTTGGG AAGACAAGCT TCCTTTATGA AGCTCTGAAA AAAGCGGATA TTGACATCTA	180
TCCTGAATTT ACTGGTACGG TGACTGAAAG TTTGCTTCAA CCATCACCCA AGGTGAGTCA	240
TGAACCAGAA CAGGTTTATC AGGTGGCGCG TGATGGCATT GCTAAGCAGG ATCATCTAGC	300
CTATCTCAAA CCCATGCTTT ATCAAAACAC CTATGCTGTA GCTGTTCCGA AAAAGATTGC	360
TCAAGAATAT GGCTTGAAGA CCATTTTCAGA CTTGAAAAAA GTGGAAGGGC AGTTGAAGGC	420
AGGTTTTTACA CTCGAGTTTA ACGACCGTGA AGATGGAAT AAGGGCTTGC AATCAATGTA	480
TGGTCTCAAT CTCAATGTAG CGACCATTGA GCCAGCCCTT CGCTATCAGG CTATTCAGTC	540
AGGGGATATT CAAATCACGG ATGCCTATTG GACTGATGCG GAATTGGAGC GTTATGATT	600
ACAGGCTCTG GAAGATGACA AGCAACTCTT CCCACCTTAT CAAGGGGCTC CACTCATGAA	660
AGAAGCTCTT CTCAAGAAAC ACCCAGAGTT GGAAGAGTT CTTAATACAT TGGCTGGTAA	720
GATTACAGAA AGCCAGATGA GCCAGCTCAA CTACCAAGTC GGTGTTGAAG GCAAGTCAGC	780
AAAGCAAGTA GCCAAGGAGT TTCTCCAAGA ACAAGGTTTG TTGAAGAAA	829

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 amino acids
- (B) TYPE: amino acid

09765272.012601

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

Gln Lys Glu Lys Glu Asn Leu Val Ile Ala Gly Lys Ile Gly Pro Glu
 1 5 10 15
 Pro Glu Ile Leu Ala Asn Met Tyr Lys Leu Leu Ile Glu Glu Asn Thr
 20 25 30
 Ser Met Thr Ala Thr Val Lys Pro Asn Phe Gly Lys Thr Ser Phe Leu
 35 40 45
 Tyr Glu Ala Leu Lys Lys Gly Asp Ile Asp Ile Tyr Pro Glu Phe Thr
 50 55 60
 Gly Thr Val Thr Glu Ser Leu Leu Gln Pro Ser Pro Lys Val Ser His
 65 70 75 80
 Glu Pro Glu Gln Val Tyr Gln Val Ala Arg Asp Gly Ile Ala Lys Gln
 85 90 95
 Asp His Leu Ala Tyr Leu Lys Pro Met Ser Tyr Gln Asn Thr Tyr Ala
 100 105 110
 Val Ala Val Pro Lys Lys Ile Ala Gln Glu Tyr Gly Leu Lys Thr Ile
 115 120 125
 Ser Asp Leu Lys Lys Val Glu Gly Gln Leu Lys Ala Gly Phe Thr Leu
 130 135 140
 Glu Phe Asn Asp Arg Glu Asp Gly Asn Lys Gly Leu Gln Ser Met Tyr
 145 150 155 160
 Gly Leu Asn Leu Asn Val Ala Thr Ile Glu Pro Ala Leu Arg Tyr Gln
 165 170 175
 Ala Ile Gln Ser Gly Asp Ile Gln Ile Thr Asp Ala Tyr Ser Thr Asp
 180 185 190
 Ala Glu Leu Glu Arg Tyr Asp Leu Gln Val Leu Glu Asp Asp Lys Gln
 195 200 205
 Leu Phe Pro Pro Tyr Gln Gly Ala Pro Leu Met Lys Glu Ala Leu Leu
 210 215 220
 Lys Lys His Pro Glu Leu Glu Arg Val Leu Asn Thr Leu Ala Gly Lys
 225 230 235 240
 Ile Thr Glu Ser Gln Met Ser Gln Leu Asn Tyr Gln Val Gly Val Glu
 245 250 255
 Gly Lys Ser Ala Lys Gln Val Ala Lys Glu Phe Leu Gln Glu Gln Gly
 260 265 270
 Leu Leu Lys Lys
 275

(2) INFORMATION FOR SEQ ID NO: 135:

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 712 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:

ACGTTCTATT GAGGACCACT TTGATTCAAA CTTCGAATTG GAATATAACC TCAAAGAAAA	60
AGGGAACA GATCTTTTGA AGCTAGTTGA TAAACAAC GACATGCGTC TGCATTTTAT	120
CCGCCAACT CATCCACGCG GTCTCGGAGA TGCTGTTTGG CAAGCCAAGG CTTTCGTCGG	180
AAATGAACCT TTGTGCTTA TGCTTGGTGA TGACTTGATG GATATCACAG ACGAAAAGGC	240
TGTTCACCTT ACCAACAAC TCATGGATGA CTACGAGCGT ACCCAGCGT CTACTATCGC	300
TGTCATGCCA GTCCTCATG ACGAAGTATC TGCTTACGGG GTTATTGCTC CGCAAGGCGA	360
AGGAAAAGAT GGCTTTTACA GTGTTGAAAC CTTTGTGAA AAACCAGCTC CAGAGGACGC	420
TCCTAGCGAC CTGCTATTA TCGGACGCTA CCTCCTCACG CCTGAAATTT TTGAGATTCT	480
CGAAAACAA GCTCCAGGTG CAGGAAATGA AATTGAGCTG ACAGATGCAA TCGACACCTT	540
CAATAAACA CAACGTGTAT TTGCTCGTGA GTTCAAAGGG GCTCGTTACG ATGTCGGAGA	600
CAAGTTTGGC TTCATGAAAA CATCCATCGA CTACGCCCTC AACACCCAC AAGTCAAAGA	660
TGATTTGAAG AATTACCTCA TCCAATTGG AAAAGAATTG ACTGAGAAGG AA	712

(2) INFORMATION FOR SEQ ID NO:136:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 237 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

Arg Ser Ile Glu Asp His Phe Asp Ser Asn Phe Glu Leu Glu Tyr Asn	
1 5 10 15	
Leu Lys Glu Lys Gly Lys Thr Asp Leu Leu Lys Leu Val Asp Lys Thr	
20 25 30	
Thr Asp Met Arg Leu His Phe Ile Arg Gln Thr His Pro Arg Gly Leu	
35 40 45	
Gly Asp Ala Val Leu Gln Ala Lys Ala Phe Val Gly Asn Glu Pro Phe	
50 55 60	
Val Val Met Leu Gly Asp Asp Leu Met Asp Ile Thr Asp Glu Lys Ala	
65 70 75 80	

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Val Pro Leu Thr Lys Gln Leu Met Asp Asp Tyr Glu Arg Thr His Ala
85 90 95

Ser Thr Ile Ala Val Met Pro Val Pro His Asp Glu Val Ser Ala Tyr
100 105 110

Gly Val Ile Ala Pro Gln Gly Glu Gly Lys Asp Gly Leu Tyr Ser Val
115 120 125

Glu Thr Phe Val Glu Lys Pro Ala Pro Glu Asp Ala Pro Ser Asp Leu
130 135 140

Ala Ile Ile Gly Arg Tyr Leu Leu Thr Pro Glu Ile Phe Glu Ile Leu
145 150 155 160

Glu Lys Gln Ala Pro Gly Ala Gly Asn Glu Ile Gln Leu Thr Asp Ala
165 170 175

Ile Asp Thr Leu Asn Lys Thr Gln Arg Val Phe Ala Arg Glu Phe Lys
180 185 190

Gly Ala Arg Tyr Asp Val Gly Asp Lys Phe Gly Phe Met Lys Thr Ser
195 200 205

Ile Asp Tyr Ala Leu Lys His Pro Gln Val Lys Asp Asp Leu Lys Asn
210 215 220

Tyr Leu Ile Gln Leu Gly Lys Glu Leu Thr Glu Lys Glu
225 230 235

(2) INFORMATION FOR SEQ ID NO: 137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 502 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:

CGCTCAAAAT ACCAGAGGTG TTCAGCTAAT CGAGCACGTT TCTCCTCAAA TGTTGAAAGC 60

CCAATTGGAG AGTGTCTTTT CTGATATTCC ACCTCAGGCT GTAAAAACTG GAATGTTGGC 120

TACTACTGAA ATCATGGAAA TCATCCAACC CTATCTTAAA AACTGGGATT GTCCCTATGT 180

CCTTGATCCT GTTATGGTTG CTACAAGTGG AGATGCCTTG ATTGACTCAA ATGCTAGAGA 240

CTATCTCAAA ACAAACTTAC TACCTCTAGC AACTATTATT ACGCCAAATC TTCCTGAAGC 300

AGAAGAGATT GTTGGTTTTT CAATCCATGA CCCCGAAGAC ATGCAGCGTG CTGGTCGCCT 360

GAATTTTAAA GAATTTGGTC CTCAGTCTGT GGTATACAAA GCGGACATC TCAAAGGTGG 420

TGCTAAAGAT TTCCTCTTTA CCAAGAATGA ACAATTTGTC TGGGAAAGCC CACGAATTCA 480

AACCTGTCAC ACCCATGGTA CT 502

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

```

Ala Gln Asn Thr Arg Gly Val Gln Leu Ile Glu His Val Ser Pro Gln
 1             5             10
Met Leu Lys Ala Gln Leu Glu Ser Val Phe Ser Asp Ile Pro Pro Gln
      20             25             30
Ala Val Lys Thr Gly Met Leu Ala Thr Thr Glu Ile Met Glu Ile Ile
      35             40             45
Gln Pro Tyr Leu Lys Lys Leu Asp Cys Pro Tyr Val Leu Asp Pro Val
      50             55             60
Met Val Ala Thr Ser Gly Asp Ala Leu Ile Asp Ser Asn Ala Arg Asp
 65             70             75             80
Tyr Leu Lys Thr Asn Leu Leu Pro Leu Ala Thr Ile Ile Thr Pro Asn
      85             90             95
Leu Pro Glu Ala Glu Glu Ile Val Gly Phe Ser Ile His Asp Pro Glu
      100            105            110
Asp Met Gln Arg Ala Gly Arg Leu Ile Leu Lys Glu Phe Gly Pro Gln
      115            120            125
Ser Val Val Ile Lys Gly Gly His Leu Lys Gly Gly Ala Lys Asp Phe
      130            135            140
Leu Phe Thr Lys Asn Glu Gln Phe Val Trp Glu Ser Pro Arg Ile Gln
 145            150            155            160
Thr Cys His Thr His Gly Thr
      165
  
```

(2) INFORMATION FOR SEQ ID NO: 139:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 805 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

```

AATTGTACAA TTAGAAAAG ATAGCAAATC AGACAAAGAA CAAGTTGATA AACTATTGGA      60
ATCATTIGAT GCATCTTCAG ATGAATCTAT TTCTAAATTA AAAGAACTAT CTGAAACTTC      120
ACTTAAACC  GATGCAGGTA AAGACTATCT TAATAACAAA GTCAAAGAAT CATCTAAGC      180
AATTGTAGAT TTTCATTGTC AAAAAGGTTT GGCTTAGAT GTTAAAGATT CAGATGACAA      240
  
```

ATTTAAAGAT AAAGCAACTC TTGAAACAAA TGTAAGAGAA ATTACAAAAC AAATGTGATT 300
 TATCAAAAAA GTTGATGAAA CTTTTAAACA AGAGAATTTG GAAGAACTC TTAATCTCT 360
 AAATGATCTT GTTGATAAAT ATCAAAAACA AATCGAAGCTT TTGAAGAAAG AAGAAGAAAA 420
 AGCTGCTGAA AAAGCTGCTG AAAAAGCAAA GGAATCTTCT AGTCAAAGTA ATTCTTCTGG 480
 TAGTGCTTCT AATGAGTCTT ATAATGGATC TTCCAATTCA AATGTAGATT ATAGTTCATC 540
 TGAACAAACT AATGGATATT CAAATAATTA TGGCGSTCAA GATTATTCTG GTTCAGGAGA 600
 TAGTTCAACA AATGGTGGAT CATCAGAACA ATATTCACTCT AGCAATTCAA ACAGCGGAGC 660
 AAATAATGTC TACAGATATA AAGGCACTGG TGCTGACGGC TATCAAAGAT ACTACTACAA 720
 AGATCATAAT AATGGAGATG TGTATGATGA CGATGGAAT TACCTTGGGA ACTTTGGTGG 780
 CGGCATTGCA GAACCTAGTC AACGC 805

(2) INFORMATION FOR SEQ ID NO:140:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 268 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

Ile Val Gln Leu Glu Lys Asp Ser Lys Ser Asp Lys Glu Gln Val Asp
 1 5 10 15
 Lys Leu Phe Glu Ser Phe Asp Ala Ser Ser Asp Glu Ser Ile Ser Lys
 20 25 30
 Leu Lys Glu Leu Ser Glu Thr Ser Leu Lys Thr Asp Ala Gly Lys Asp
 35 40 45
 Tyr Leu Asn Asn Lys Val Lys Glu Ser Ser Lys Ala Ile Val Asp Phe
 50 55 60
 His Leu Gln Lys Gly Leu Ala Tyr Asp Val Lys Asp Ser Asp Asp Lys
 65 70 75 80
 Phe Lys Asp Lys Ala Thr Leu Glu Thr Asn Val Lys Glu Ile Thr Lys
 85 90 95
 Gln Ile Asp Phe Ile Lys Lys Val Asp Glu Thr Phe Lys Gln Glu Asn
 100 105 110
 Leu Glu Glu Thr Leu Lys Ser Leu Asn Asp Leu Val Asp Lys Tyr Gln
 115 120 125
 Lys Gln Ile Glu Leu Leu Lys Lys Glu Glu Glu Lys Ala Ala Glu Lys
 130 135 140
 Ala Ala Glu Lys Ala Lys Glu Ser Ser Ser Gln Ser Asn Ser Ser Gly
 145 150 155 160

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Ser Ala Ser Asn Glu Ser Tyr Asn Gly Ser Ser Asn Ser Asn Val Asp
 165 170 175

Tyr Ser Ser Ser Glu Gln Thr Asn Gly Tyr Ser Asn Asn Tyr Gly Gly
 180 185 190

Gln Asp Tyr Ser Gly Ser Gly Asp Ser Ser Thr Asn Gly Gly Ser Ser
 195 200 205

Glu Gln Tyr Ser Ser Ser Asn Ser Asn Ser Gly Ala Asn Asn Val Tyr
 210 215 220

Arg Tyr Lys Gly Thr Gly Ala Asp Gly Tyr Gln Arg Tyr Tyr Tyr Lys
 225 230 235 240

Asp His Asn Asn Gly Asp Val Tyr Asp Asp Asp Gly Asn Tyr Leu Gly
 245 250 255

Asn Phe Gly Gly Gly Ile Ala Glu Pro Ser Gln Arg
 260 265

(2) INFORMATION FOR SEQ ID NO: 141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 211 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141:

TCTGACCAAG CAAAAGAAG CAGTCAATGA CAAAGGAAAA GCAGCTGTTG TTAAGGTGGT 60

GGAAAGCCAG GCAGAACTTT ATAGCTTAGA AAAGAATGAA GATGCTAGCC TAAGAAAGTT 120

ACAAGCAGAT GGACGCATCA CGGAAGAACA GGCTAAAGCT TATAAAGAAT ACAATGATAA 180

AAATGGAGGA GCAAATCGTA AAGTCAATGA T 211

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

Leu Thr Lys Gln Lys Glu Ala Val Asn Asp Lys Gly Lys Ala Ala Val
 1 5 10 15

Val Lys Val Val Glu Ser Gln Ala Glu Leu Tyr Ser Leu Glu Lys Asn
 20 25 30

Glu Asp Ala Ser Leu Arg Lys Leu Gln Ala Asp Gly Arg Ile Thr Glu
 35 40 45

Glu Gln Ala Lys Ala Tyr Lys Glu Tyr Asn Asp Lys Asn Gly Gly Ala
 50 55 60

Asn Arg Lys Val Asn Asp
 65 70

(2) INFORMATION FOR SEQ ID NO: 143:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 331 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:

GTCCGGCTCT GTCCAGTCCA CTTTTCAGC GGTAGAGGAA CAGATTTTCT TTAIGGAGTT	60
TGAAGAACT TATCGGGAAA CCAAAAAACG CAGTGTAGCC AGTCAGCAA AGACTAGTCT	120
GAAGTAGAT GGCAGACGC TTAGCAATGG CAGTCAAAG TTGCCAGTCC CTAAGGAAT	180
TCAGGCCCA TCAGGCCAA GTATTACATT TGACCGAGCT GGGGGCAATT CGTCCCTGGC	240
TAAGGTTGAA TTTGAGCCA GTAAAGGAGC GATTGCGTAT CAATTATATC TAGGAAATGG	300
AAAAATTAAA CGCATTAAGG AAACAAAAA T	331

(2) INFORMATION FOR SEQ ID NO:144:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 110 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

Ser Gly Ser Val Gln Ser Thr Phe Ser Ala Val Glu Glu Gln Ile Phe	
1 5 10 15	
Phe Met Glu Phe Glu Glu Leu Tyr Arg Glu Thr Gln Lys Arg Ser Val	
20 25 30	
Ala Ser Gln Gln Lys Thr Ser Leu Asn Leu Asp Gly Gln Thr Leu Ser	
35 40 45	
Asn Gly Ser Gln Lys Leu Pro Val Pro Lys Gly Ile Gln Ala Pro Ser	
50 55 60	
Gly Gln Ser Ile Thr Phe Asp Arg Ala Gly Gly Asn Ser Ser Leu Ala	
65 70 75 80	
Lys Val Glu Phe Gln Thr Ser Lys Gly Ala Ile Arg Tyr Gln Leu Tyr	
85 90 95	
Leu Gly Asn Gly Lys Ile Lys Arg Ile Lys Glu Thr Lys Asn	
100 105 110	

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(2) INFORMATION FOR SEQ ID NO: 145:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 196 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145:

```
GGGACAAATT CAAAAAATA GCGAAGAGGA AGCAAAATC TTGCAAAAGG AAGAAGTCTT      60
GAGGGTAGCT AAGATGGCCC TGCAGACGGG GCAAAATCAG GTAAGCATCA ACGGAGTTGA      120
GATTTCAGGTA TTTTCTAGTG AAAAAGGATT GGAGGTCTAC CATGGTTCAG AACAGTTGTT      180
GGCAATCAAA GAGCCA                                     196
```

(2) INFORMATION FOR SEQ ID NO:146:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 65 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

```
Gly Gln Ile Gln Lys Asn Arg Gln Glu Glu Ala Lys Ile Leu Gln Lys
 1             5             10             15
Glu Glu Val Leu Arg Val Ala Lys Met Ala Leu Gln Thr Gly Gln Asn
 20             25             30
Gln Val Ser Ile Asn Gly Val Glu Ile Gln Val Phe Ser Ser Glu Lys
 35             40             45
Gly Leu Glu Val Tyr His Gly Ser Glu Gln Leu Leu Ala Ile Lys Glu
 50             55             60
Pro
65
```

(2) INFORMATION FOR SEQ ID NO: 147:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 319 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147: - - - -

```
TCGCTACCAG CAACAAAGCG AGCAAAAGGA GTGGCTCTTG TTTGTGGAAC AACTTGAGGT      60
```

AGAATTAGAC CGTTCGCAGT TCGAAAAAGT AGAAGGCAAT CGCCTATACA TGAAGCAAGA	120
TGGCAAGGAC ATCGCCATCG GTAAGTCAAA GTCAGATGAT TTCCGTAAAA CGAATGCTCG	180
TGGTCGAGGT TATCAGCCTA TGGTTTATGG ACTCAAATCT GTACGGATTA CAGAGGACAA	240
TCAACTGGTT CGCTTTCATT TCCAGTTCCA AAAAGGCTTA GAAAGGGAGT TCATCTATCG	300
TGTGGAAAAA GAAAAAAGT	319

(2) INFORMATION FOR SEQ ID NO:148:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 106 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

Arg Tyr Gln Gln Gln Ser Glu Gln Lys Glu Trp Leu Leu Phe Val Asp	
1 5 10 15	
Gln Leu Glu Val Glu Leu Asp Arg Ser Gln Phe Glu Lys Val Glu Gly	
20 25 30	
Asn Arg Leu Tyr Met Lys Gln Asp Gly Lys Asp Ile Ala Ile Gly Lys	
35 40 45	
Ser Lys Ser Asp Asp Phe Arg Lys Thr Asn Ala Arg Gly Arg Gly Tyr	
50 55 60	
Gln Pro Met Val Tyr Gly Leu Lys Ser Val Arg Ile Thr Glu Asp Asn	
65 70 75 80	
Gln Leu Val Arg Phe His Phe Gln Phe Gln Lys Gly Leu Glu Arg Glu	
85 90 95	
Phe Ile Tyr Arg Val Glu Lys Glu Lys Ser	
100 105	

(2) INFORMATION FOR SEQ ID NO: 149:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 322 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:

GAACCGACAA GTCGCCCACT ATCAAGACTA TGCTTTGAAT AAAGAAAAAT TGGTTGCTTT	60
TGCTATGGCT AAACGAACCA AAGATAAGGT TGAGCAAGAA AGTGGGGAAC AGTTTTTTAA	120
TCTAGTCTAG GTAAGCTATC AAAACAAGAA AACTGGCTTA GTGACGAGGG TTCGTACGGA	180
TAAGAGCCAA TATGAGTTTC TGTTCCTTC AGTCAAAATC AAAGAAGAGA AAAGAGATAA	240

AAAGGAAGAG GTAGCGACCG ATTCAAGCGA AAAAGTGGAG AAGAAAAAAT CAGAAGAGAA 300
GCCTGAAAAG AAAGAGAATT CA 322

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

Asn Arg Gln Val Ala His Tyr Gln Asp Tyr Ala Leu Asn Lys Glu Lys
1 5 10 15
Leu Val Ala Phe Ala Met Ala Lys Arg Thr Lys Asp Lys Val Glu Gln
20 25 30
Glu Ser Gly Glu Gln Phe Phe Asn Leu Gly Gln Val Ser Tyr Gln Asn
35 40 45
Lys Lys Thr Gly Leu Val Thr Arg Val Arg Thr Asp Lys Ser Gln Tyr
50 55 60
Glu Phe Leu Phe Pro Ser Val Lys Ile Lys Glu Glu Lys Arg Asp Lys
65 70 75 80
Lys Glu Glu Val Ala Thr Asp Ser Ser Glu Lys Val Glu Lys Lys Lys
85 90 95
Ser Glu Glu Lys Pro Glu Lys Lys Glu Asn Ser
100 105

(2) INFORMATION FOR SEQ ID NO: 151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 784 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151:

GGTTGTGCGC TGGCAATATA TCCCGTTTCC ATCTAAAGGT AGTACAATTG GTCCCTTACCC 60
AAATGGTATC AGATTAGAAG GTTTTCCAAA GTCAGAGTGG TACTACTTCG ATAAAAATGG 120
AGTGCTACAA GAGTTTGTGG GTTGAAAAAC ATTAGAGATT AAAACTAAAG ACAGTGTTGG 180
AAGAAAGTAC GGGGAAAAAC GTGAAGATTG AGAAGATAAA GAAGAGAAGC GTTATTATAC 240
GAAGTATTAC TTTAATCAAA ATCATTCTTT AGAGACAGGT TGGCTTTATG ATCAGTCTAA 300
CTGTGATTAT CTAGCTAAGA CGGAAATTAA TGGAGAAAAA TACCTTGGTG GTGAAAGACG 360

TGCGGGGTGG ATAAACGATG ATTCGACTTG GTACTACCTA GATCCAACAA CTGGTATTAT	420
GCAACAGGT TGGCAATATC TAGGTAATAA GTGGTACTAC CTCCGTTCTT CAGGAGCAAT	480
GGCCACTGGC TGGTATCAGG AAGGTACCAC TTGGTATTAT TTAGACCACC CAAATGGCGA	540
TATGAAAAA GGTGGGAAA ACCTTGGGAA CAAATGGTAC TATCTCCGTT CATCAGGAGC	600
TATGGCAACT GGTGGTATC AAGATGGTTC AACTTGGTAC TACCTAAATG CAGGTAATGG	660
AGACATGAAG ACAGGTTGGT TCCAGGTCAA TGGCAACTGG TACTATGCTT ATAGCTCAGG	720
TGCTTTGGCA GTGAATACGA CCGTAGATGG CTATTCTGTC AACTATAATG GCGAATGGGT	780
TCGG	784

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

Val	Val	Gly	Trp	Gln	Tyr	Ile	Pro	Phe	Pro	Ser	Lys	Gly	Ser	Thr	Ile
1				5					10					15	
Gly	Pro	Tyr	Pro	Asn	Gly	Ile	Arg	Leu	Glu	Gly	Phe	Pro	Lys	Ser	Glu
			20					25					30		
Trp	Tyr	Tyr	Phe	Asp	Lys	Asn	Gly	Val	Leu	Gln	Glu	Phe	Val	Gly	Trp
		35					40					45			
Lys	Thr	Leu	Glu	Ile	Lys	Thr	Lys	Asp	Ser	Val	Gly	Arg	Lys	Tyr	Gly
	50					55					60				
Glu	Lys	Arg	Glu	Asp	Ser	Glu	Asp	Lys	Glu	Glu	Lys	Arg	Tyr	Tyr	Thr
65					70					75					80
Asn	Tyr	Tyr	Phe	Asn	Gln	Asn	His	Ser	Leu	Glu	Thr	Gly	Trp	Leu	Tyr
				85					90					95	
Asp	Gln	Ser	Asn	Trp	Tyr	Tyr	Leu	Ala	Lys	Thr	Glu	Ile	Asn	Gly	Glu
			100					105					110		
Asn	Tyr	Leu	Gly	Gly	Glu	Arg	Arg	Ala	Gly	Trp	Ile	Asn	Asp	Asp	Ser
		115					120					125			
Thr	Trp	Tyr	Tyr	Leu	Asp	Pro	Thr	Thr	Gly	Ile	Met	Gln	Thr	Gly	Trp
	130					135					140				
Gln	Tyr	Leu	Gly	Asn	Lys	Trp	Tyr	Tyr	Leu	Arg	Ser	Ser	Gly	Ala	Met
145					150					155					160
Ala	Thr	Gly	Trp	Tyr	Gln	Glu	Gly	Thr	Thr	Trp	Tyr	Tyr	Leu	Asp	His
			165						170				175		
Pro	Asn	Gly	Asp	Met	Lys	Thr	Gly	Trp	Gln	Asn	Leu	Gly	Asn	Lys	Trp

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260

180 185 190

Tyr Tyr Leu Arg Ser Ser Gly Ala Met Ala Thr Gly Trp Tyr Gln Asp
 195 200 205

Gly Ser Thr Trp Tyr Tyr Leu Asn Ala Gly Asn Gly Asp Met Lys Thr
 210 215 220

Gly Trp Phe Gln Val Asn Gly Asn Trp Tyr Tyr Ala Tyr Ser Ser Gly
 225 230 235 240

Ala Leu Ala Val Asn Thr Thr Val Asp Gly Tyr Ser Val Asn Tyr Asn
 245 250 255

Gly Glu Trp Val Arg
 260

(2) INFORMATION FOR SEQ ID NO: 153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1708 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

GGCCAAATCA GAATGGGTAG AAGACAAGGG AGCCTTTTAT TATCTTGACC AAGATGGAAA	60
GATGAAAGA AATGCTTGGG TAGGAACCTC CTATGTTGGT GCAACAGGTG CCAAAGTAAT	120
AGAAGACTGG GTCTATGATT CTCAATACGA TGCTTGGTTT TATATCAAAG CAGATGGACA	180
GCACGCAGAG AAAGAATGGC TCCAAATTAA AGGGAAGGAC TATTATTTC AATCCGGTGG	240
TTATCTACTG ACAAGTCAGT GGATTAATCA AGCTTATGTG AATGCTAGTG GTGCCAAAGT	300
ACAGCAAGGT TGGCTTTTGG ACAAACAATA CCAATCTTGG TTTTACATCA AAGAAAATGG	360
AAACTATGCT GATAAAGAAT GGATTTTCGA GAATGGTCAC TATTATTATC TAAATCCGG	420
TGGCTACATG GCAGCCAATG AATGGATTGG GGATAAGGAA TCCTGGTTTT ATCTCAAATT	480
TGATGGGAAA ATGGCTGAAA AAGAATGGGT CTACGATTCT CATAGTCAAG CTGTGTTACTA	540
CTTCAAATCC GGTGGTTTACA TGACAGCCAA TGAATGGATT TGGGATAAGG AATCTTGGTT	600
TTATCTCAAA TCTGATGGGA AAATAGCTGA AAAAGAATGG GTCTACGATT CTCATAGTCA	660
AGCTTGGTAC TACTTCAAAT CCGGTGGTTA CATGACAGCC AATGAATGGA TTTGGGATAA	720
GGAATCTTGG TTTTACCTCA AATCTGATGG GAAATAGCT GAAAAGAAT GGGCTACGA	780
TTCTCATAGT CAAGCTTGGT ACTACTTCAA ATCTGGTGGC TACATGGCGA AAAATGAGAC	840
AGTAGATGGT TATCAGCTTG GAAGCGATGG TAAATGGCTT GGAGGAAAAA CTACAAATGA	900
AAATGCTGCT TACTATCAAG TAGTGCCTGT TACAGCCAAT GTTTATGATT CAGATGGTGA	960
AAAGCTTTCC TATATATCGC AAGGTAGTGT CGTATGGCTA GATAAGGATA GAAAAAGTGA	1020

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TGACAAGCGC TTGGCTATTA CTATTCTCGG TTTGTCAGGC TATATGAAAA CAGAAGATT 1080
 ACAAGCGCTA GATGCTAGTA AGGACTTTAT CCCTTATTAT GAGAGTGATG GCCACCGTTT 1140
 TTATCACTAT GTGGCTCAGA ATGCTAGTAT CCCAGTAGCT TCTCATCTTT CTGATATGGA 1200
 AGTAGGCAAG AAATATTATT CGGCAGATGG CCTGCATTTT GATGTTTTTA AGCTTGAGAA 1260
 TCCCTTCCTT TTCAAAGATT TAACAGAGGC TACAACTAC AGTGTGAAG AATTGGATAA 1320
 GGTATTAGT TTGCTAAACA TTAACAATAG CCTTTTGAGG AACAAAGGCG CTACTTTTAA 1380
 GGAAGCCGAA GAACATTACC ATATCAATGC TCTTTATCTC CTGCCCATA GTGCCCTAGA 1440
 AAGTAACCTG GGAAGAAGTA AAATTGCCAA AGATAAGAAT AATTTCTTTG GCATTACAGC 1500
 CTATGATACG ACCCCTTACC TTTCTGCTAA GACATTGAT GATGTGGATA AGGGAATTTT 1560
 AGGTGCAACC AAGTGGATTA AGGAAAATTA TATCGATAGG GGAAGAACTT TCCTTGGA 1620
 CAAGGCTCTT GGTATGAATG TGAATATGCT TTCAGACCTT TATTGGGGCG AAAAAATTGC 1680
 TAGTGTGATG ATGAAATCA ATGAGAAG 1708

(2) INFORMATION FOR SEQ ID NO:154:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 569 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

Ala Lys Ser Glu Trp Val Glu Asp Lys Gly Ala Phe Tyr Tyr Leu Asp
 1 5 10 15
 Gln Asp Gly Lys Met Lys Arg Asn Ala Trp Val Gly Thr Ser Tyr Val
 20 25 30
 Gly Ala Thr Gly Ala Lys Val Ile Glu Asp Trp Val Tyr Asp Ser Gln
 35 40 45
 Tyr Asp Ala Trp Phe Tyr Ile Lys Ala Asp Gly Gln His Ala Glu Lys
 50 55 60
 Glu Trp Leu Gln Ile Lys Gly Lys Asp Tyr Tyr Phe Lys Ser Gly Gly
 65 70 75 80
 Tyr Leu Leu Thr Ser Gln Trp Ile Asn Gln Ala Tyr Val Asn Ala Ser
 85 90 95
 Gly Ala Lys Val Gln Gln Gly Trp Leu Phe Asp Lys Gln Tyr Gln Ser
 100 105 110
 Trp Phe Tyr Ile Lys Glu Asn Gly Asn Tyr Ala Asp Lys Glu Trp Ile
 115 120 125
 Phe Glu Asn Gly His Tyr Tyr Leu Lys Ser Gly Tyr Met Ala
 130 135 140

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Ala Asn Glu Trp Ile Trp Asp Lys Glu Ser Trp Phe Tyr Leu Lys Phe
145 150 155 160

Asp Gly Lys Met Ala Glu Lys Glu Trp Val Tyr Asp Ser His Ser Gln
165 170 175

Ala Trp Tyr Tyr Phe Lys Ser Gly Gly Tyr Met Thr Ala Asn Glu Trp
180 185 190

Ile Trp Asp Lys Glu Ser Trp Phe Tyr Leu Lys Ser Asp Gly Lys Ile
195 200 205

Ala Glu Lys Glu Trp Val Tyr Asp Ser His Ser Gln Ala Trp Tyr Tyr
210 215 220

Phe Lys Ser Gly Gly Tyr Met Thr Ala Asn Glu Trp Ile Trp Asp Lys
225 230 235 240

Glu Ser Trp Phe Tyr Leu Lys Ser Asp Gly Lys Ile Ala Glu Lys Glu
245 250 255

Trp Val Tyr Asp Ser His Ser Gln Ala Trp Tyr Tyr Phe Lys Ser Gly
260 265 270

Gly Tyr Met Ala Lys Asn Glu Thr Val Asp Gly Tyr Gln Leu Gly Ser
275 280 285

Asp Gly Lys Trp Leu Gly Gly Lys Thr Thr Asn Glu Asn Ala Ala Tyr
290 295 300

Tyr Gln Val Val Pro Val Thr Ala Asn Val Tyr Asp Ser Asp Gly Glu
305 310 315 320

Lys Leu Ser Tyr Ile Ser Gln Gly Ser Val Val Trp Leu Asp Lys Asp
325 330 335

Arg Lys Ser Asp Asp Lys Arg Leu Ala Ile Thr Ile Ser Gly Leu Ser
340 345 350

Gly Tyr Met Lys Thr Glu Asp Leu Gln Ala Leu Asp Ala Ser Lys Asp
355 360 365

Phe Ile Pro Tyr Tyr Glu Ser Asp Gly His Arg Phe Tyr His Tyr Val
370 375 380

Ala Gln Asn Ala Ser Ile Pro Val Ala Ser His Leu Ser Asp Met Glu
385 390 395 400

Val Gly Lys Lys Tyr Tyr Ser Ala Asp Gly Leu His Phe Asp Gly Phe
405 410 415

Lys Leu Glu Asn Pro Phe Leu Phe Lys Asp Leu Thr Glu Ala Thr Asn
420 425 430

Tyr Ser Ala Glu Glu Leu Asp Lys Val Phe Ser Leu Leu Asn Ile Asn
435 440 445

Asn Ser Leu Leu Glu Asn Lys Gly Ala Thr Phe Lys Glu Ala Glu Glu
450 455 460

His Tyr His Ile Asn Ala Leu Tyr Leu Leu Ala His Ser Ala Leu Glu
465 470 475 480

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Ser Asn Trp Gly Arg Ser Lys Ile Ala Lys Asp Lys Asn Asn Phe Phe
 485 490 495

Gly Ile Thr Ala Tyr Asp Thr Thr Pro Tyr Leu Ser Ala Lys Thr Phe
 500 505 510

Asp Asp Val Asp Lys Gly Ile Leu Gly Ala Thr Lys Trp Ile Lys Glu
 515 520 525

Asn Tyr Ile Asp Arg Gly Arg Thr Phe Leu Gly Asn Lys Ala Ser Gly
 530 535 540

Met Asn Val Glu Tyr Ala Ser Asp Pro Tyr Trp Gly Glu Lys Ile Ala
 545 550 555 560

Ser Val Met Met Lys Ile Asn Glu Lys
 565

(2) INFORMATION FOR SEQ ID NO: 155:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 946 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155:

ATTTCGAGAT GATTCTGAAG GATGGCAGTT TGTCCAAGAA AATGGTAGAA CCTACTACAA	60
AAAGGGGGAT CTAAAGAAA CCTACTGGAG AGTGATAGAT GGGAAGTACT ATTATTTTGA	120
TCCTTTATCC GGAGAGATGG TTGTCGGCTG GCAATATATA CCTGCTCCAC ACAAGGGGGT	180
TACGATTGGT CCTTCTCCAA GAATAGAGAT TGCTCTTAGA CCAGATTGGT TTTATTTTGG	240
TCAAGATGGT GTATTACAAG AATTTGTTGG CAAGCAAGTT TTAGAAGCAA AAACCTGTAC	300
GAATACCAAC AAACATCATG GGAAGAATA TGATAGCCAA GCAGAGAAAC GAGTCTATTA	360
TTTGAAGAT CAGCGTAGTT ATCATACTTT AAAAACTGGT TGGATTTATG AAGAGGGTCA	420
TTGGTATTAT TTACAGAAGG ATGGTGGCTT TGATTCGCGC ATCAACAGAT TGACGGTTGG	480
AGAGCTAGCA CGTGGTTGGG TTAAGGATTA CCCTCTTACG TATGATGAAG AGAAGCTAAA	540
AGCAGCTCCA TGGTACTATC TAAATCCAGC AACTGGCATT ATGCAACAG GTTGSCAATA	600
TCTAGGTAAT AGATGGTACT ACCTCCATTC GTCAGGAGCT ATGGCAACTG GCTGGTATAA	660
GGAAGGCTCA ACTTGGTACT ATCTAGATGC TGAAGATGGT GATATGAGAA CTGGCTGGCA	720
AAACCTTGGG AACAAATGGT ACTATCTCCG TTCATCAGGA GCTATGGCAA CTGGTTGGTA	780
TCAGGAAAGT TCGACTTGGT ACTATCTAAA TGCAAGTAAT GGAGATATGA AAACAGGCTG	840
GTTCCAAGTC AATGGTAACT GGTACTATGC CTATGATTCA GGTGCTTTAG CTGTAAATAC	900
CACAGTAGGT GGTACTACT TAACTATAA TGGTGAATGG GTTAAAG	946

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(2) INFORMATION FOR SEQ ID NO:156:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 316 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

```

Val Phe Ala Asp Asp Ser Glu Gly Trp Gln Phe Val Gln Glu Asn Gly
 1             5             10             15

Arg Thr Tyr Tyr Lys Lys Gly Asp Leu Lys Glu Thr Tyr Trp Arg Val
      20             25             30

Ile Asp Gly Lys Tyr Tyr Tyr Phe Asp Pro Leu Ser Gly Glu Met Val
      35             40             45

Val Gly Trp Gln Tyr Ile Pro Ala Pro His Lys Gly Val Thr Ile Gly
 50             55             60

Pro Ser Pro Arg Ile Glu Ile Ala Leu Arg Pro Asp Trp Phe Tyr Phe
65             70             75             80

Gly Gln Asp Gly Val Leu Gln Glu Phe Val Gly Lys Gln Val Leu Glu
      85             90             95

Ala Lys Thr Ala Thr Asn Thr Asn Lys His His Gly Glu Glu Tyr Asp
      100            105            110

Ser Gln Ala Glu Lys Arg Val Tyr Tyr Phe Glu Asp Gln Arg Ser Tyr
      115            120            125

His Thr Leu Lys Thr Gly Trp Ile Tyr Glu Glu Gly His Trp Tyr Tyr
      130            135            140

Leu Gln Lys Asp Gly Gly Phe Asp Ser Arg Ile Asn Arg Leu Thr Val
      145            150            155            160

Gly Glu Leu Ala Arg Gly Trp Val Lys Asp Tyr Pro Leu Thr Tyr Asp
      165            170            175

Glu Glu Lys Leu Lys Ala Ala Pro Trp Tyr Tyr Leu Asn Pro Ala Thr
      180            185            190

Gly Ile Met Gln Thr Gly Trp Gln Tyr Leu Gly Asn Arg Trp Tyr Tyr
      195            200            205

Leu His Ser Ser Gly Ala Met Ala Thr Gly Trp Tyr Lys Glu Gly Ser
      210            215            220

Thr Trp Tyr Tyr Leu Asp Ala Glu Asn Gly Asp Met Arg Thr Gly Trp
      225            230            235            240

Gln Asn Leu Gly Asn Lys Trp Tyr Tyr Leu Arg Ser Ser Gly Ala Met
      245            250            255

Ala Thr Gly Trp Tyr Gln Glu Ser Ser Thr Trp Tyr Tyr Leu Asn Ala
      260            265            270

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(2) INFORMATION FOR SEQ ID NO: 157:

(A) LENGTH: 1415 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

TGTCGCTGCA	AATGAAACTG	AAGTAGCAAA	AACCTTCGCAG	GATACAACGA	CAGCTTCAAG	60
TAGTTTCAGAG	CAAAATCAGT	CTTCTAATAA	AACGCAARAC	AGCGCAGAAG	TACAGACTAA	120
TGCTGCTGCC	CACTGGGATG	GGGATTATTA	TGTAAGGATG	GATGGTTCTA	AAGCTCAAA	180
TGAATGGATT	TTTGACAAC	ACTATAAGCG	TTGGTTTTAT	ATTAATTCAG	ATGGTCGTTA	240
CTCGCAGAAT	GAATGGCATG	GAAATTACTA	CCTGAAATCA	GGTGGATATA	TGGCCCAAAA	300
CGAGTGGATC	TATGACAGTA	ATTACAAGAG	TTGGTTTTAT	CTCAAGTCAG	ATGGGGCTTA	360
TGCTCATCAA	GAATGGCAAT	TGATTGGAAA	TAAGTGGTAC	TACTTCAAGA	AGTGGGGTTA	420
CATGGCTAAA	AGCCAATGGC	AAGGAAGTTA	TTTCTTGAA	GGTCAAGGAG	CTATGATGCA	480
AAATGAATGG	CTSCATGAT	CCAGCCTATT	CTGCTTATTT	TTATCTAAAA	TCCGATGGAA	540
CTTATGCTAA	CCAAGAGTGG	CAAAAAGTGG	GCGGCAAAAT	GTACTATTTT	AAGAAGTGGG	600
GCTATATGGC	TCGGAATGAG	TGGCAAGGCA	ACTACTATTT	GACTGGAAGT	GGTGCCATGG	660
CGACTGACGA	AGTGATTATG	GATGGTACTC	GCTATATCTT	TGCGCCCTCT	GGTGAGCTCA	720
AAGAAAAAAA	AGATTTGAAT	GTCGGCTGGG	TTCACAGAGA	TGTAAGCGC	TATTTCTTTA	780
ATAATAGAGA	AGAACAAGTG	GGAACCGAAC	ATGCTAAGAA	AGTCATTGAT	ATTAGTGAGC	840
ACAATGGTCG	TATCAATGAT	TGGA AAAAGG	TTATTGATGA	GAACGAAGTG	GATGGTGTC	900
TTGTTCTGCT	AGGTTATAGC	GGTAAGAAAG	ACAAGGAATT	GGCGCATAA	ATTAAGGAGT	960
TAAACCGCTC	GGGAATTCCT	TATGGTGCTC	ATCTCTATAC	CTATGCTGAA	AATGAGACCG	1020
ATGCTGAGAG	TGACGCTAAA	CAGACCATTG	AACCTATAAA	GAAATACAAT	ATGAACCTGT	1080
CTTACCCATAT	CTATTATGAT	GTTGAGAATT	GGGAATATGT	AAATAAGAGC	AAGAGAGCTC	1140
CAAGTGATAC	AGGCACCTGG	GTTAAAAATCA	TCAACAAGTA	CATGGACACG	ATGAAGCAGG	1200
CGGGTTATCA	AAATGTGTAT	GTCTATAGCT	ATCGTAGTTT	ATTACAGACG	CGTTTAAAAAC	1260

ACCCAGATAT TTAAAAACAT GTAAACTGGG TAGCGGCCTA TACGAATGCT TTAGAATGGG 1320
 AAAACCCCTCA TTATTCAGGA AAAAAAGGTT GGCAATATAC CTCTTCTGAA TACATGAAAG 1380
 GAATCCAAGG GCGCGTAGAT GTCAGCGTTT GGTAT 1415

(2) INFORMATION FOR SEQ ID NO:158:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 471 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

Val	Ala	Ala	Asn	Glu	Thr	Glu	Val	Ala	Lys	Thr	Ser	Gln	Asp	Thr	Thr	1	5	10	15
Thr	Ala	Ser	Ser	Ser	Ser	Glu	Gln	Asn	Gln	Ser	Ser	Asn	Lys	Thr	Gln	20	25	30	
Thr	Ser	Ala	Glu	Val	Gln	Thr	Asn	Ala	Ala	Ala	His	Trp	Asp	Gly	Asp	35	40	45	
Tyr	Tyr	Val	Lys	Asp	Asp	Gly	Ser	Lys	Ala	Gln	Ser	Glu	Trp	Ile	Phe	50	55	60	
Asp	Asn	Tyr	Tyr	Lys	Ala	Trp	Phe	Tyr	Ile	Asn	Ser	Asp	Gly	Arg	Tyr	65	70	75	80
Ser	Gln	Asn	Glu	Trp	His	Gly	Asn	Tyr	Tyr	Leu	Lys	Ser	Gly	Gly	Tyr	85	90	95	
Met	Ala	Gln	Asn	Glu	Trp	Ile	Tyr	Asp	Ser	Asn	Tyr	Lys	Ser	Trp	Phe	100	105	110	
Tyr	Leu	Lys	Ser	Asp	Gly	Ala	Tyr	Ala	His	Gln	Glu	Trp	Gln	Leu	Ile	115	120	125	
Gly	Asn	Lys	Trp	Tyr	Tyr	Phe	Lys	Lys	Trp	Gly	Tyr	Met	Ala	Lys	Ser	130	135	140	
Gln	Trp	Gln	Gly	Ser	Tyr	Phe	Leu	Asn	Gly	Gln	Gly	Ala	Met	Met	Gln	145	150	155	160
Asn	Glu	Trp	Leu	Tyr	Asp	Pro	Ala	Tyr	Ser	Ala	Tyr	Phe	Tyr	Leu	Lys	165	170	175	
Ser	Asp	Gly	Thr	Tyr	Ala	Asn	Gln	Glu	Trp	Gln	Lys	Val	Gly	Gly	Lys	180	185	190	
Trp	Tyr	Tyr	Phe	Lys	Lys	Trp	Gly	Tyr	Met	Ala	Arg	Asn	Glu	Trp	Gln	195	200	205	
Gly	Asn	Tyr	Tyr	Leu	Thr	Gly	Ser	Gly	Ala	Met	Ala	Thr	Asp	Glu	Val	210	215	220	
Ile	Met	Asp	Gly	Thr	Arg	Tyr	Ile	Phe	Ala	Ala	Ser	Gly	Glu	Leu	Lys				

225	230	235	240
Glu Lys Lys Asp	Leu Asn Val Gly Trp	Val His Arg Asp Gly Lys Arg	
245		250	255
Tyr Phe Phe Asn Asn Arg Glu Glu Gln Val Gly Thr Glu His Ala Lys			
260	265		270
Lys Val Ile Asp Ile Ser Glu His Asn Gly Arg Ile Asn Asp Trp Lys			
275	280		285
Lys Val Ile Asp Glu Asn Glu Val Asp Gly Val Ile Val Arg Leu Gly			
290	295		300
Tyr Ser Gly Lys Glu Asp Lys Glu Leu Ala His Asn Ile Lys Glu Leu			
305	310		315
Asn Arg Leu Gly Ile Pro Tyr Gly Val Tyr Leu Tyr Thr Tyr Ala Glu			
325		330	335
Asn Glu Thr Asp Ala Glu Ser Asp Ala Lys Gln Thr Ile Glu Leu Ile			
340	345		350
Lys Lys Tyr Asn Met Asn Leu Ser Tyr Pro Ile Tyr Tyr Asp Val Glu			
355	360		365
Asn Trp Glu Tyr Val Asn Lys Ser Lys Arg Ala Pro Ser Asp Thr Gly			
370	375		380
Thr Trp Val Lys Ile Ile Asn Lys Tyr Met Asp Thr Met Lys Gln Ala			
385	390		395
Gly Tyr Gln Asn Val Tyr Val Tyr Ser Tyr Arg Ser Leu Leu Gln Thr			
405		410	415
Arg Leu Lys His Pro Asp Ile Leu Lys His Val Asn Trp Val Ala Ala			
420	425		430
Tyr Thr Asn Ala Leu Glu Trp Glu Asn Pro His Tyr Ser Gly Lys Lys			
435	440		445
Gly Trp Gln Tyr Thr Ser Ser Glu Tyr Met Lys Gly Ile Gln Gly Arg			
450	455		460
Val Asp Val Ser Val Trp Tyr			
465	470		

(2) INFORMATION FOR SEQ ID NO: 159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1924 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159:

TACGTCCTCAG CCTACTTTTG TAAGAGCAGA AGAATCTCCA CAAGTTGTGCG AAAAATCTTC	60
ATTAGAGAAG AAATATGAGG AAGCAAAAGC AAAAGCTGAT ACTGCCAAGA AAGATTACGA	120

AACGGCTAAA AAGAAAGCAG AAGACGCTCA GAAAAAGTAT GAAGATGATC AGAAGAGAAC	180
TGAGGAGAAA GCTCGAAAAG AAGCAGAAGC ATCTCAAAAA TTGAATGATG TGGCGCTTGT	240
TGTTCAAAAT GCATATAAAG AGTACCGAGA AGTTCAAAAT CAACGTAGTA AATATAAATC	300
TGACGCTGAA TATCAGAAAA AATTAACAGA GGTGACTCT AAAATAGAGA AGGCTAGGAA	360
AGAGCAACAG GACTTGCAAA ATAAATTTAA TGAAGTAAGA GCAGTTGTAT TTCTGAACC	420
AAATGCGTTG GCTGAGACTA AGAAAAAAGC AGAAGAAGCT AAAGCAGAAG AAAAGTAGC	480
TAAGAGAAAA TATGATTATG CAACTCTAAA GGTAGCTACT GCGAAGAAAG AAGTAGAGSC	540
TAAGGAACCT GAAATTGAAA AACTTCAATA TGAATTTCT ACTTTGGAAC AAGAAGTTGC	600
TACTGCTCAA CATCAAGTAG ATAATTGAA AAAACTTCTT GCTGGTGGG ATCTCTGATGA	660
TGGCACAGAA GTTATAGAAG CTAAATTAAA AAAAGGAGAA GCTGAGCTAA ACGCTAAACA	720
AGCTGAGTTA GCAAAAAAAC AAACAGAAGT TGA AAAACTT CTTGACAGCC TTGATCCTGA	780
AGGTAAGACT CAGGATGAAT TAGATAAAGA AGCAGAAGAA GCTGAGTTGG ATAAAAAAGC	840
TGATGAACCT CAAAATAAAG TTGCTGATT AGAAAAAGAA ATTAGTAACT TTGAAATATT	900
ACTTGGAGGG GCTGATNCTG AAGATGATAC TGCTGCTCTT CAAAATAAAT TAGCTACTAA	960
AAAAGCTGAA TTGAAAAAAA CTCAAAAAGA ATTAGATGCA GCTCTTAATG AGTTAGGCC	1020
TGATGGAGAT GAAGAAGAAA CTCACGCGCC GGCTCCTCAA CCAGAGCAAC CAGCTCCTGC	1080
ACCAAAACCA GAGCAACCAG CTCACGCTCC AAAACCAGAG CAACCAGCTC CTGCACCAAA	1140
ACCAGAGCAA CCAGCTCCAG CTCCAAACC AGAGCAACCA GCTCCAGCTC CAAAACCAGA	1200
GCAACCAGCT AAGCCGAGA AACCAGCTGA AGAGCCTACT CAACCAGAAA AACCAGCCAC	1260
TCCAAAAACA GGCTGGAAC AAGAAAACGG TATGTGGTAT TTCTACAATA CTGATGGTTC	1320
AATGGCAATA GGTGGCTCC AAAACAACGG TTCATGGTAC TACCTAAACG CTAACGGCGC	1380
TATGGCAACA GGTGGGTGA AAGATGAGA TACCTGGTAC TATCTTGAG CATCAGGTGC	1440
TATGAAAGCA AGCCAATGGT TCAAAGTATC AGATAAATGG TACTATGTCA ACAGCAATGG	1500
CGTATGGCG ACAGGCTGGC TCCAATACAA TGGCTCATGG TACTACCTCA ACGCTAATGG	1560
TGATATGGCG ACAGGATGGC TCCAATACAA CGGTTCATGG TATTACCTCA ACGCTAATGG	1620
TGATATGGCG ACAGGATGGC TCAAAGTCAA CGGTTCATGG TACTACCTAA ACGCTAACGG	1680
TGCTATGGCT ACAGGTTGGG CTAAGTCAA CGGTTCATGG TACTACCTAA ACGCTAACGG	1740
TTCAATGGCA ACAGGTTGGG TGAAGATGG AGATACCTGG TACTATCTTG AAGCATCAGG	1800
TGCTATGAAA GCAAGCCAAT GGTTCAAAGT ATCAGATAAA TGGTACTATG TCAATGGCTT	1860
AGGTGCCCTT GCAGTCAACA CAACTGTAGA TGGCTATAAA GTCAATGCCA ATGGTGAATG	1920
GGTT	1924

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 641 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

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Thr Ser Gln Pro Thr Phe Val Arg Ala Glu Glu Ser Pro Gln Val Val
1      5      10      15

Glu Lys Ser Ser Leu Glu Lys Lys Tyr Glu Glu Ala Lys Ala Lys Ala
20     25     30

Asp Thr Ala Lys Lys Asp Tyr Glu Thr Ala Lys Lys Lys Ala Glu Asp
35     40     45

Ala Gln Lys Lys Tyr Glu Asp Asp Gln Lys Arg Thr Glu Glu Lys Ala
50     55     60

Arg Lys Glu Ala Glu Ala Ser Gln Lys Leu Asn Asp Val Ala Leu Val
65     70     75     80

Val Gln Asn Ala Tyr Lys Glu Tyr Arg Glu Val Gln Asn Gln Arg Ser
85     90     95

Lys Tyr Lys Ser Asp Ala Glu Tyr Gln Lys Lys Leu Thr Glu Val Asp
100    105    110

Ser Lys Ile Glu Lys Ala Arg Lys Glu Gln Gln Asp Leu Gln Asn Lys
115    120    125

Phe Asn Glu Val Arg Ala Val Val Val Pro Glu Pro Asn Ala Leu Ala
130    135    140

Glu Thr Lys Lys Lys Ala Glu Glu Ala Lys Ala Glu Glu Lys Val Ala
145    150    155    160

Lys Arg Lys Tyr Asp Tyr Ala Thr Leu Lys Val Ala Leu Ala Lys Lys
165    170    175

Glu Val Glu Ala Lys Glu Leu Glu Ile Glu Lys Leu Gln Tyr Glu Ile
180    185    190

Ser Thr Leu Glu Gln Glu Val Ala Thr Ala Gln His Gln Val Asp Asn
195    200    205

Leu Lys Lys Leu Leu Ala Gly Ala Asp Pro Asp Asp Gly Thr Glu Val
210    215    220

Ile Glu Ala Lys Leu Lys Lys Gly Glu Ala Glu Leu Asn Ala Lys Gln
225    230    235    240

Ala Glu Leu Ala Lys Lys Gln Thr Glu Leu Glu Lys Leu Leu Asp Ser
245    250    255

Leu Asp Pro Glu Gly Lys Thr Gln Asp Glu Leu Asp Lys Glu Ala Glu
260    265    270

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Glu Ala Glu Leu Asp Lys Lys Ala Asp Glu Leu Gln Asn Lys Val Ala
 275 280 285
 Asp Leu Glu Lys Glu Ile Ser Asn Leu Glu Ile Leu Leu Gly Gly Ala
 290 295 300
 Asp Xaa Glu Asp Asp Thr Ala Ala Leu Gln Asn Lys Leu Ala Thr Lys
 305 310 315 320
 Lys Ala Glu Leu Glu Lys Thr Gln Lys Glu Leu Asp Ala Ala Leu Asn
 325 330 335
 Glu Leu Gly Pro Asp Gly Asp Glu Glu Glu Thr Pro Ala Pro Ala Pro
 340 345 350
 Gln Pro Glu Gln Pro Ala Pro Ala Pro Lys Pro Glu Gln Pro Ala Pro
 355 360 365
 Ala Pro Lys Pro Glu Gln Pro Ala Pro Ala Pro Lys Pro Glu Gln Pro
 370 375 380
 Ala Pro Ala Pro Lys Pro Glu Gln Pro Ala Pro Ala Pro Lys Pro Glu
 385 390 395 400
 Gln Pro Ala Lys Pro Glu Lys Pro Ala Glu Glu Pro Thr Gln Pro Glu
 405 410 415
 Lys Pro Ala Thr Pro Lys Thr Gly Trp Lys Gln Glu Asn Gly Met Trp
 420 425 430
 Tyr Phe Tyr Asn Thr Asp Gly Ser Met Ala Ile Gly Trp Leu Gln Asn
 435 440 445
 Asn Gly Ser Trp Tyr Tyr Leu Asn Ala Asn Gly Ala Met Ala Thr Gly
 450 455 460
 Trp Val Lys Asp Gly Asp Thr Trp Tyr Tyr Leu Glu Ala Ser Gly Ala
 465 470 475 480
 Met Lys Ala Ser Gln Trp Phe Lys Val Ser Asp Lys Trp Tyr Tyr Val
 485 490 495
 Asn Ser Asn Gly Ala Met Ala Thr Gly Trp Leu Gln Tyr Asn Gly Ser
 500 505 510
 Trp Tyr Tyr Leu Asn Ala Asn Gly Asp Met Ala Thr Gly Trp Leu Gln
 515 520 525
 Tyr Asn Gly Ser Trp Tyr Tyr Leu Asn Ala Asn Gly Asp Met Ala Thr
 530 535 540
 Gly Trp Ala Lys Val Asn Gly Ser Trp Tyr Tyr Leu Asn Ala Asn Gly
 545 550 555 560
 Ala Met Ala Thr Gly Trp Ala Lys Val Asn Gly Ser Trp Tyr Tyr Leu
 565 570 575
 Asn Ala Asn Gly Ser Met Ala Thr Gly Trp Val Lys Asp Gly Asp Thr
 580 585 590
 Trp Tyr Tyr Leu Glu Ala Ser Gly Ala Met Lys Ala Ser Gln Trp Phe
 595 600 605

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Lys Val Ser Asp Lys Trp Tyr Tyr Val Asn Gly Leu Gly Ala Leu Ala
610 615 620

Val Asn Thr Thr Val Asp Gly Tyr Lys Val Asn Ala Asn Gly Glu Trp
625 630 635 640

Val

(2) INFORMATION FOR SEQ ID NO: 161:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 670 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:

TGACACAGTG AAGGTCATG CTACATTGTG GAAATCCATG ACAACTGAAA TGTACCAAGA 60
 ACAACAGAAC CATTCTCTCG CCTACAATCA ACGCTTGNT TCGCAAAATC GCATTGTAGA 120
 TCCTTTTTTG CGGAGGGAT ATGAGGTCAA TTACCAAGTG TCTGACGACC CTGATGCAGT 180
 CTATGGTTAC TTGTCATTTC CAAGTTTGGA AATCATGGAG CCGGTTTATT TGGGAGCAGA 240
 TTATCATCAT TTAGGGATGG GCTTGGGTCA TGTGGATGGT ACACCGCTGC CTCTGGATGG 300
 TACAGGGATT CGCTCAGTGA TTGCTGGGCA CCGTGCAGAG CCAAGCCATG TCTTTTCCG 360
 CCATTGGAT CAGCTAAAAG TTGGAGATGC TCTTTATTAT GATAATGGCC AGGAAATTGT 420
 AGAATATCAG ATGATGGACA CAGAGATTAT TTTACCGTCG GAATGGGAAA AATTAGAATC 480
 GGTTAGCTCT AAAAATATCA TGACCTTGAT AACCTGCGAT CCGATTCCTA CCTTTAATAA 540
 ACGCTTATTA GTGAATTTTG AACGAGTCGC TGTATTATCA AAATCAGATC CACAACACGC 600
 TGCAGTTGCG AGGTTTGCTT TTACGAAAGA AGGACAATCT GTATCGCGTG TTGCAACCTC 660
 TCAATGGTTG 670

(2) INFORMATION FOR SEQ ID NO:162:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 223 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

Gly Gln Val Lys Gly His Ala Thr Phe Val Lys Ser Met Thr Thr Glu
 1 5 10 15
 Met Tyr Gln Glu Gln Asn His Ser Leu Ala Tyr Asn Gln Arg Leu
 20 25 30

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Xaa Ser Gln Asn Arg Ile Val Asp Pro Phe Leu Ala Glu Gly Tyr Glu
 35 40 45
 Val Asn Tyr Gln Val Ser Asp Asp Pro Asp Ala Val Tyr Gly Tyr Leu
 50 55 60
 Ser Ile Pro Ser Leu Glu Ile Met Glu Pro Val Tyr Leu Gly Ala Asp
 65 70 75 80
 Tyr His His Leu Gly Met Gly Leu Ala His Val Asp Gly Thr Pro Leu
 85 90 95
 Pro Leu Asp Gly Thr Gly Ile Arg Ser Val Ile Ala Gly His Arg Ala
 100 105 110
 Glu Pro Ser His Val Phe Phe Arg His Leu Asp Gln Leu Lys Val Gly
 115 120 125
 Asp Ala Leu Tyr Tyr Asp Asn Gly Gln Glu Ile Val Glu Tyr Gln Met
 130 135 140
 Met Asp Thr Glu Ile Ile Leu Pro Ser Glu Trp Glu Lys Leu Glu Ser
 145 150 155 160
 Val Ser Ser Lys Asn Ile Met Thr Leu Ile Thr Cys Asp Pro Ile Pro
 165 170 175
 Thr Phe Asn Lys Arg Leu Leu Val Asn Phe Glu Arg Val Ala Val Tyr
 180 185 190
 Gln Lys Ser Asp Pro Gln Thr Ala Ala Val Ala Arg Val Ala Phe Thr
 195 200 205
 Lys Glu Gly Gln Ser Val Ser Arg Val Ala Thr Ser Gln Trp Leu
 210 215 220

(2) INFORMATION FOR SEQ ID NO: 163:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 784 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163:

TATTGCTCCTT TGAAGGATT TGAGAGAAAC CATGTTGGAA ATTGCTTCTG GTGCTCAAAA	60
TCTTCGTGCC AAGGAAGTTG GTGCCTATGA ACTGAGAGAA GTAACTCGCC AATTAAATGC	120
TATGTTGGAT CAGATTGATC AGTTGATGGT AGCTATTCTG AGCCAGGAAG AACGACCCG	180
TCAGTACCAA CTCAAGCCC TTTGAGCCA GATTAATCCA CATTTCTCTT ATAACACTTT	240
GGACACATC ATCTGGATGG CTGAATTCA TGATAGTCAG CGAGTGGTGC AGGTGACCAA	300
GTCCTTGGCA ACCTATTTC GCTTGCGCT CAATCAAGGC AAGACTTGA TTTGTCTCTC	360
TGACGAAATC AATCATGTCC GCCAGTATCT CTTTATCCAG AAACAACGCT ATGGAGATAA	420

GCTGGAATAC GAAATTAATG AAAATGITGC CTTTGATAAT TTAGTCTTAC CCAAGCTGGT	480
CCTACAACCC CTTGTAGAAA ATGCTCTTTA CCATGGCATT AAGGAAAAGG AAGTTCAGGG	540
CCATATTAAA CTTTCTGTCC AGAAACAGGA TTCGGGATTG GTCATCCGTA TTGAGGATGA	600
TGGCGTGGC TTCCAAGATG CTGGTGATAG TAGTCAAAGT CAACTCAAAC GTGGGGGAGT	660
TGTTCTTCAA AATGTCGATC AACGGCTCAA ACTTCATTTT GGAGCCAATT ACCATATGAA	720
GATTGATTCT AGACCCCAAA AAGGGACGAA AGTTGAAATA TATATAAATA GAATAGAAAC	780
TAGC	784

(2) INFORMATION FOR SEQ ID NO:164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

Ile	Ala	Pro	Leu	Lys	Asp	Leu	Arg	Glu	Thr	Met	Leu	Glu	Ile	Ala	Ser	1	5	10	15
Gly	Ala	Gln	Asn	Leu	Arg	Ala	Lys	Glu	Val	Gly	Ala	Tyr	Glu	Leu	Arg	20	25	30	
Glu	Val	Thr	Arg	Gln	Phe	Asn	Ala	Met	Leu	Asp	Gln	Ile	Asp	Gln	Leu	35	40	45	
Met	Val	Ala	Ile	Arg	Ser	Gln	Glu	Glu	Thr	Thr	Arg	Gln	Tyr	Gln	Leu	50	55	60	
Gln	Ala	Leu	Ser	Ser	Gln	Ile	Asn	Pro	His	Phe	Leu	Tyr	Asn	Thr	Leu	65	70	75	80
Asp	Thr	Ile	Ile	Trp	Met	Ala	Glu	Phe	His	Asp	Ser	Gln	Arg	Val	Val	85	90	95	
Gln	Val	Thr	Lys	Ser	Leu	Ala	Thr	Tyr	Phe	Arg	Leu	Ala	Leu	Asn	Gln	100	105	110	
Gly	Lys	Asp	Leu	Ile	Cys	Leu	Ser	Asp	Glu	Ile	Asn	His	Val	Arg	Gln	115	120	125	
Tyr	Leu	Phe	Ile	Gln	Lys	Gln	Arg	Tyr	Gly	Asp	Lys	Leu	Glu	Tyr	Glu	130	135	140	
Ile	Asn	Glu	Asn	Val	Ala	Phe	Asp	Asn	Leu	Val	Leu	Pro	Lys	Leu	Val	145	150	155	160
Leu	Gln	Pro	Leu	Val	Glu	Asn	Ala	Leu	Tyr	His	Gly	Ile	Lys	Glu	Lys	165	170	175	
Glu	Gly	Gln	Gly	His	Ile	Lys	Leu	Ser	Val	Gln	Lys	Gln	Asp	Ser	Gly	180	185	190	

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Leu Val Ile Arg Ile Glu Asp Asp Gly Val Gly Phe Gln Asp Ala Gly
 195 200 205
 Asp Ser Ser Gln Ser Gln Leu Lys Arg Gly Gly Val Gly Leu Gln Asn
 210 215 220
 Val Asp Gln Arg Leu Lys Leu His Phe Gly Ala Asn Tyr His Met Lys
 225 230 235 240
 Ile Asp Ser Arg Pro Gln Lys Gly Thr Lys Val Glu Ile Tyr Ile Asn
 245 250 255
 Arg Ile Glu Thr Ser
 260

(2) INFORMATION FOR SEQ ID NO: 165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:

TAGGTCATAT GGGACTTTTT TTCTACAACA AATAGGCTC CATAATATCT ATAAGGGATT	60
TACCCACTAC AAATATTATA GAGCCGAAAA TTCACATCTA ATATATGCAG ACTACTTTGA	120
AATGAAATTA AAAAAATTAT TAAAGGATGA CACAAAAGTT TTTGAAAAAT CTACATTCAA	180
ATTGTGAGAA GGATATAAAA TATACCTGAC AGAATCTAAA GAATCTGGAA TTAACAAAT	240
GGACAATGTC ATAAATATAT TTGAGTTTAT TGAATCTAAA AGTATTGCTT TATATTTTCA	300
AAAACGATTA AATGAGCTGA TAGAT	325

(2) INFORMATION FOR SEQ ID NO:166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

Arg Ser Tyr Gly Thr Phe Phe Leu Gln Gln Asn Arg Leu His Asn Ile
 1 5 10 15
 Tyr Lys Gly Phe Thr His Tyr Lys Tyr Tyr Arg Ala Glu Asn Ser His
 20 25 30
 Leu Ile Tyr Ala Asp Tyr Phe Glu Met Lys Leu Lys Lys Leu Leu Lys
 35 40 45
 Asp Asp Thr Lys Val Phe Glu Lys Ser Thr Phe Lys Phe Val Glu Gly
 50 55 60

Tyr Lys Ile Tyr Leu Thr Glu Ser Lys Glu Ser Gly Ile Lys Gln Met
65 70 75 80

Asp Asn Val Ile Lys Tyr Phe Glu Phe Ile Glu Ser Lys Ser Ile Ala
85 90 95

Leu Tyr Phe Gln Lys Arg Leu Asn Glu Leu Ile Asp
100 105

(2) INFORMATION FOR SEQ ID NO: 167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 238 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167:

CAACGTTGAG AATTATTTCG GAATGTGTTT GGATAGCATT CAGAATCAGA CGTATCAAAA	60
TTTGTAGTGT TTATTAAATCA ATGATGGCTC TCCAGATCAT TCATCCAAAA TATGTGAAGA	120
ATTTGTAGAG AAAGATTCTC GTTTCAAATA TTTTGAGAAA GCAAACGGCG GTCTTTCATC	180
AGCTCGTAAC CTAGGTATTG ARTGTTTCGG GGGGGGCGTA CATTACTTTT GTAGACTC	238

(2) INFORMATION FOR SEQ ID NO:168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

Asn Val Glu Asn Tyr Leu Arg Met Cys Leu Asp Ser Ile Gln Asn Gln	
1 5 10 15	
Thr Tyr Gln Asn Phe Glu Cys Leu Ile Asn Asp Gly Ser Pro Asp	
20 25 30	
His Ser Ser Lys Ile Cys Glu Glu Phe Val Glu Lys Asp Ser Arg Phe	
35 40 45	
Lys Tyr Phe Glu Lys Ala Asn Gly Gly Leu Ser Ser Ala Arg Asn Leu	
50 55 60	
Gly Ile Glu Cys Ser Gly Gly Gly Val His Tyr Phe Cys Arg Leu	
65 70 75	

(2) INFORMATION FOR SEQ ID NO: 169:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 742 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:

CTACTATCAA TCAAGTTCTT CAGCCATTGA GGCCACCATT GAGGGCAACA GCCAAACGAC	60
CATCAGCCAG ACTAGCCACT TTATTGAGTC TTATATCAAA AACTAGAAA CCACCTCGAC	120
TGGTTTGACC CAGCAGACGG ATGTTCTGGC CTATGCTGAG AATCCGAGTC AAGACAAGGT	180
CGAGGGAATC CGAGATTTGT TTTTGACCAT CTGGAAGTCA GATAAGGACT TGAAAACGTG	240
TGTGCTGGTG ACCAAATCTG GTCAGGTCAT TTCTACAGAT GACAGTGTGC AGATGAAAAC	300
TTCTCTGAT ATGATGGCTG AGGATTGGTA CCAAAGGCC ATTCATCAGG GAGCTATGCC	360
TGTTTGAATC CCAGCTCGTA AATCAGATAG TCAGTGGGTC ATTTCTGTCA CTCAAGAACT	420
TGTTGATGCA AAGGGAGCCA ATCTGGTGT GCTTCGTTG GATATTCTT ATGAAACTCT	480
GGAAGCCTAT CTCAATCAAC TCCAGTTGGG GCAGCAGGGC TTGCTTCA TTATCAATGA	540
AAACCATGAA TTTGCTTACC ATCCTCAACA CACAGTTTAT AGTTCGCTA GCAAATGGA	600
GGCTATGAAA CCCTACATCG ATACAGGTCA GGGTTATACT CCTGGTCACA AATCCTACGT	660
CAGTCAAGAG AAGATTGCGA GAACTGATTG GACGGTGCTT GCGGTGTCAT CATTGGAAAA	720
GTTAGACCAG GTTCGGAGTC AG	742

(2) INFORMATION FOR SEQ ID NO:170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 247 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

Tyr	Tyr	Gln	Ser	Ser	Ser	Ser	Ala	Ile	Glu	Ala	Thr	Ile	Glu	Gly	Asn
1				5					10					15	
Ser	Gln	Thr	Thr	Ile	Ser	Gln	Thr	Ser	His	Phe	Ile	Gln	Ser	Tyr	Ile
			20					25					30		
Lys	Lys	Leu	Glu	Thr	Thr	Ser	Thr	Gly	Leu	Thr	Gln	Gln	Thr	Asp	Val
		35					40				45				
Leu	Ala	Tyr	Ala	Glu	Asn	Pro	Ser	Gln	Asp	Lys	Val	Glu	Gly	Ile	Arg
	50				55					60					
Asp	Leu	Phe	Leu	Thr	Ile	Leu	Lys	Ser	Asp	Lys	Asp	Leu	Lys	Thr	Val
65					70					75				80	
Val	Leu	Val	Thr	Lys	Ser	Gly	Gln	Val	Ile	Ser	Thr	Asp	Asp	Ser	Val
			85					90						95	

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Gln Met Lys Thr Ser Ser Asp Met Met Ala Glu Asp Trp Tyr Gln Lys
100 105 110

Ala Ile His Gln Gly Ala Met Pro Val Leu Thr Pro Ala Arg Lys Ser
115 120 125

Asp Ser Gln Trp Val Ile Ser Val Thr Gln Glu Leu Val Asp Ala Lys
130 135 140

Gly Ala Asn Leu Gly Val Leu Arg Leu Asp Ile Ser Tyr Glu Thr Leu
145 150 155 160

Glu Ala Tyr Leu Asn Gln Leu Gln Leu Gly Gln Gln Gly Phe Ala Phe
165 170 175

Ile Ile Asn Glu Asn His Glu Phe Val Tyr His Pro Gln His Thr Val
180 185 190

Tyr Ser Ser Ser Ser Lys Met Glu Ala Met Lys Pro Tyr Ile Asp Thr
195 200 205

Gly Gln Gly Tyr Thr Pro Gly His Lys Ser Tyr Val Ser Gln Glu Lys
210 215 220

Ile Ala Gly Thr Asp Trp Thr Val Leu Gly Val Ser Ser Leu Glu Lys
225 230 235 240

Leu Asp Gln Val Arg Ser Gln
245

(2) INFORMATION FOR SEQ ID NO: 171:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1282 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

GACAAAAACA TTAAACGTC CTGAGGTTTT ATCACTGCA GGGACTTTAG AGAAGCTAAA	60
GGTAGCTGTT CAGTATGGAG CAGATGCTGT CTTTATCGGT GGTCAAGCCT ATGTTCTTTCG	120
TAGCCGTGCG GGAAACTTTA CTTTCGAACA GATGGAAGAA GCGGTGCAGT TTGCGGCCAA	180
GTATGTTGCC AAGGTCTATG TAGCGGCTAA TATGGTTATG CACGAAGGAA ATGAAGCTGG	240
TGCTGTTGAG TGGTCCGTA AACTGCGTGA TATCGGGATT GCAGCAGTTA TCGTATCTGA	300
CCCAGCCTTG ATTATGATTG CAGTGACTGA AGCACCAGGC CTTGAAATCC ACCTTTCTAC	360
CCAAGCCAGT GCCACTAACT ATGAAACCCT TGAGTTCTGG AAAGAGCTAG GCTTGACTCG	420
TGTCGTTTTA GCGCGTGAGG TTTCAATGGA AGAATTAGCT GAGATCCGCA AACGTACAGA	480
TGTTGAAATT GAAGCCTTTG TCCATGGAGC TATGTGTATT TCATACTCTG GACGTTGTAC	540
TCCTTCAAAC CACATGAGTA TCGGTGATGC CAACCGTGGT GGATGTTCTC AGTCATGCCG	600

TTGGAAATAC GACCTTTACG ATATGCCATT TGGGAAAGAA CGTAAGAGTT TGCAGGGTGA 660
 GATTCCAGAA GAATTTTCAA TGTCAGCCGT TGACATGTCT ATGATTGACC ANATTCCAGA 720
 TATGATTGAA AATGGTGTGG ACAGTCTAAA AATCGAAGGA CGTATGNAGT CTATTCACATA 780
 NGTATCAACA GTAACCAACT GCTACAAGGC GGCTGTGGAT GCCTATCTTG AAAGTCCTGA 840
 AAAGTTTGAA GCTATCAAAC AAGACTTGGT GGACGAGATG TGAAGGTTG CCCAACGTGA 900
 ACTGGCTACA GGATTTTACT ATGGTACACC ATCTGAAAAT GAGCAGTTGT TTGGTGCTCG 960
 TCGTAAAATC CCTGAGTACA AGTTTGTGCG TGAAGTGGTT TCCTATGATG ATCGGSCACA 1020
 AACAGCAACT ATTCGTCAAC GAAACGTCAT TAACGAAGGG GACCAAGTTG AGTTTATGG 1080
 TCCAGGTTTC CGTCATTTTG AAACCTATAT TGAAGATTG CATGATGCTA AAGGCAATAA 1140
 AATCGACCGC GCTCCAAATC CAATGGAAC ATTGACTATT AAAGTCCCAC AACCTGTTCA 1200
 ATCAGGAGAC ATGGTTCGAG CTCTTAAAGA GGGGCTTATC AATCTTATA AGGAAGATGG 1260
 AACCAGCGTC ACAGTTCGTG CT 1282

(2) INFORMATION FOR SEQ ID NO:172:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 427 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

Thr Lys Thr Leu Lys Arg Pro Glu Val Leu Ser Pro Ala Gly Thr Leu
 1 5 10 15
 Glu Lys Leu Lys Val Ala Val Gln Tyr Gly Ala Asp Ala Val Phe Ile
 20 25 30
 Gly Gly Gln Ala Tyr Gly Leu Arg Ser Arg Ala Gly Asn Phe Thr Phe
 35 40 45
 Glu Gln Met Glu Glu Gly Val Gln Phe Ala Ala Lys Tyr Gly Ala Lys
 50 55 60
 Val Tyr Val Ala Ala Asn Met Val Met His Glu Gly Asn Glu Ala Gly
 65 70 75 80
 Ala Gly Glu Trp Phe Arg Lys Leu Arg Asp Ile Gly Ile Ala Ala Val
 85 90 95
 Ile Val Ser Asp Pro Ala Leu Ile Met Ile Ala Val Thr Glu Ala Pro
 100 105 110
 Gly Leu Glu Ile His Leu Ser Thr Gln Ala Ser Ala Thr Asn Tyr Glu
 115 120 125
 Thr Leu Glu Phe Trp Lys Glu Leu Gly Leu Thr Arg Val Val Leu Ala
 130 135 140

Arg Glu Val Ser Met Glu Glu Leu Ala Glu Ile Arg Lys Arg Thr Asp
 145 150 155 160
 Val Glu Ile Glu Ala Phe Val His Gly Ala Met Cys Ile Ser Tyr Ser
 165 170 175
 Gly Arg Cys Thr Leu Ser Asn His Met Ser Met Arg Asp Ala Asn Arg
 180 185 190
 Gly Gly Cys Ser Gln Ser Cys Arg Trp Lys Tyr Asp Leu Tyr Asp Met
 195 200 205
 Pro Phe Gly Lys Glu Arg Lys Ser Leu Gln Gly Glu Ile Pro Glu Glu
 210 215 220
 Phe Ser Met Ser Ala Val Asp Met Ser Met Ile Asp Xaa Ile Pro Asp
 225 230 235 240
 Met Ile Glu Asn Gly Val Asp Ser Leu Lys Ile Glu Gly Arg Met Xaa
 245 250 255
 Ser Ile His Xaa Val Ser Thr Val Thr Asn Cys Tyr Lys Ala Ala Val
 260 265 270
 Asp Ala Tyr Leu Glu Ser Pro Glu Lys Phe Glu Ala Ile Lys Gln Asp
 275 280 285
 Leu Val Asp Glu Met Trp Lys Val Ala Gln Arg Glu Leu Ala Thr Gly
 290 295 300
 Phe Tyr Tyr Gly Thr Pro Ser Glu Asn Glu Gln Leu Phe Gly Ala Arg
 305 310 315 320
 Arg Lys Ile Pro Glu Tyr Lys Phe Val Ala Glu Val Val Ser Tyr Asp
 325 330 335
 Asp Ala Ala Gln Thr Ala Thr Ile Arg Gln Arg Asn Val Ile Asn Glu
 340 345 350
 Gly Asp Gln Val Glu Phe Tyr Gly Pro Gly Phe Arg His Phe Glu Thr
 355 360 365
 Tyr Ile Glu Asp Leu His Asp Ala Lys Gly Asn Lys Ile Asp Arg Ala
 370 375 380
 Pro Asn Pro Met Glu Leu Leu Thr Ile Lys Val Pro Gln Pro Val Gln
 385 390 395 400
 Ser Gly Asp Met Val Arg Ala Leu Lys Glu Gly Leu Ile Asn Leu Tyr
 405 410 415
 Lys Glu Asp Gly Thr Ser Val Thr Val Arg Ala
 420 425

(2) INFORMATION FOR SEQ ID NO: 173:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 778 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

102200-222360

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:

TTCTCAGGAG ACCTTTAAAA ATATCACCAA TAGCTTCTCC ATGCAAAATCA ATCGTCGCGT	60
CAACCAAGGA ACGCCTCGTG GTGCTGGGAA TATCAAGGGT GAAGACATCA AAAAATCAC	120
CGAAACAAG GCCATTGAGT CTTATGTCAA ACGTATCAAC GCTATCGGAG ATTTGACTGG	180
ATATGACCTG ATTGAAACGC CAGAAACCAA GAAGAATCTC ACTGCTGATC GTGCCAAGCG	240
TTTTGGAAGT AGCTTGATGA TTACAGGTGT CAATGACTCC TCTAAAGAAG ACAAGTTTGT	300
CTCTGGTTCT TATAAACTAG TCGAAGGAGA GCACTTAACC AACGACGACA AGGATAAAAT	360
CCTCTTGCAC AAGGACTTGG CAGCCAAACA CGGCTGGAAA GTAGGGGACA AGGTTAAACT	420
GGACTCTAAT ATCTACGATG CAGATAATGA AAAAGGAGCC AAGGAAACAG TTGAAGTGAC	480
AAACAAGGGA CTCTTTGATG GTCATAATAA GTCAGCAGTA ACCTACTCAC AAGAAGTTTA	540
CGAAACACA GCTATTACAG ACATTCACAC TGCTGCAAAA CTTTATGGAT ACACAGAAGA	600
CACAGCCATT TATGGGGAGC CAACCTTCTT TGTAACAGCA GACAAGAACT TGGATGATGT	660
TATGAAGAG TTGAATGGCA TCAGTGGTAT CAACTGGAAG AGCTACACAC TCGTCAAGAG	720
CTCCTCTAAC TACCCAGCTC TTGAGCAATC TATCTCTGGT ATGTACAAGA TGGCCAAC	778

(2) INFORMATION FOR SEQ ID NO:174:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 259 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

Ser	Gln	Glu	Thr	Phe	Lys	Asn	Ile	Thr	Asn	Ser	Phe	Ser	Met	Gln	Ile
1				5				10					15		
Asn	Arg	Arg	Val	Asn	Gln	Gly	Thr	Pro	Arg	Gly	Ala	Gly	Asn	Ile	Lys
			20				25						30		
Gly	Glu	Asp	Ile	Lys	Lys	Ile	Thr	Glu	Asn	Lys	Ala	Ile	Glu	Ser	Tyr
		35				40						45			
Val	Lys	Arg	Ile	Asn	Ala	Ile	Gly	Asp	Leu	Thr	Gly	Tyr	Asp	Leu	Ile
		50			55					60					
Glu	Thr	Pro	Glu	Thr	Lys	Lys	Asn	Leu	Thr	Ala	Asp	Arg	Ala	Lys	Arg
65				70					75					80	
Phe	Gly	Ser	Ser	Leu	Met	Ile	Thr	Gly	Val	Asn	Asp	Ser	Ser	Lys	Glu
				85				90						95	
Asp	Lys	Phe	Val	Ser	Gly	Ser	Tyr	Lys	Leu	Val	Glu	Gly	Glu	His	Leu
				100				105						110	

Thr Asn Asp Asp Lys Asp Lys Ile Leu Leu His Lys Asp Leu Ala Ala
 115 120 125
 Lys His Gly Trp Lys Val Gly Asp Lys Val Lys Leu Asp Ser Asn Ile
 130 135 140
 Tyr Asp Ala Asp Asn Glu Lys Gly Ala Lys Glu Thr Val Glu Val Thr
 145 150 155 160
 Ile Lys Gly Leu Phe Asp Gly His Asn Lys Ser Ala Val Thr Tyr Ser
 165 170 175
 Gln Glu Leu Tyr Glu Asn Thr Ala Ile Thr Asp Ile His Thr Ala Ala
 180 185 190
 Lys Leu Tyr Gly Tyr Thr Glu Asp Thr Ala Ile Tyr Gly Asp Ala Thr
 195 200 205
 Phe Phe Val Thr Ala Asp Lys Asn Leu Asp Asp Val Met Lys Glu Leu
 210 215 220
 Asn Gly Ile Ser Gly Ile Asn Trp Lys Ser Tyr Thr Leu Val Lys Ser
 225 230 235 240
 Ser Ser Asn Tyr Pro Ala Leu Glu Gln Ser Ile Ser Gly Met Tyr Lys
 245 250 255
 Met Ala Asn

(2) INFORMATION FOR SEQ ID NO: 175:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 694 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 175:

AGTAAATGCG CAATCAAAATT CATTAAATATT AATAGATGAA CCTGAAATCT CACTTCATCC	60
GAGTGCAATC TATAAATTTA AAGAGTTTTT ACTTCAAGAG TGTTTAAATA AAAAACATCA	120
AATTATTATC ACTACACATT CTACACAAC TATAAAAGAT TTTCCTAGAG AAGCCGTGAA	180
ACTTTTAGTG AAAAACGGAG AAAAGGTAGA TGTATTGAA AATATTGATT ATCAGGATGC	240
ATTTTTTGAA TTAGGTGATG TGTATCATTC TAGGAAGATG ATTTATGTTG AAGATAGACT	300
AGCTAAATAT ATTCTAGAGT TTGTTATCAC TCATTCAGGT AGTGAGAATC TTAACAGAA	360
TTTAGTAGTG AGATATATTC CTGGTGGAGC AAATCAAATA ATTTGTAATA ATATTTTAAA	420
CTCATCGTAT TTAGATCCCG ATAACCATTA TTTTGGGCTT GATGGAGATC AAAACACTAA	480
TGTTAGTGAA TCAAATAATT TAATGAAC TAATTGAAAAA GGTGTTGTTA TATCAGATAA	540
AAATCTCGAA TCAGATAATA AAAATCTTGA TGATATTATA AAATTGATAA NGGGATGTCC	600

AATTAARTTT AATGTTTCAG GTAATAAAGG GCAAAAAAAT AATATTGAAT TAATTGCGAA 660
 ACAAGAAGC TTTATAGATT ATTGGGCTAA ATAC 694

(2) INFORMATION FOR SEQ ID NO:176:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 231 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

Val Asn Ala Gln Ser Asn Ser Leu Ile Leu Ile Asp Glu Pro Glu Ile
 1 5 10 15
 Ser Leu His Pro Ser Ala Ile Tyr Lys Phe Lys Glu Phe Leu Leu Gln
 20 25 30
 Glu Cys Leu Asn Lys Lys His Gln Ile Ile Ile Thr Thr His Ser Thr
 35 40 45
 Gln Leu Ile Lys Asp Phe Pro Arg Glu Ala Val Lys Leu Leu Val Lys
 50 55 60
 Asn Gly Glu Lys Val Asp Val Ile Glu Asn Ile Asp Tyr Gln Asp Ala
 65 70 75 80
 Phe Phe Glu Leu Gly Asp Val Tyr His Ser Arg Lys Met Ile Tyr Val
 85 90 95
 Glu Asp Arg Leu Ala Lys Tyr Ile Leu Glu Phe Val Ile Thr His Ser
 100 105 110
 Gly Ser Glu Asn Leu Lys Gln Asn Leu Val Val Arg Tyr Ile Pro Gly
 115 120 125
 Gly Ala Asn Gln Ile Ile Cys Asn Asn Ile Leu Asn Ser Ser Tyr Leu
 130 135 140
 Asp Ser Asp Asn His Tyr Phe Trp Leu Asp Gly Asp Gln Asn Thr Asn
 145 150 155 160
 Val Ser Glu Ser Asn Asn Leu Met Asn Tyr Leu Glu Asn Gly Val Val
 165 170 175
 Ile Ser Asp Lys Ile Pro Glu Ser Asp Asn Lys Asn Leu Asp Asp Ile
 180 185 190
 Ile Lys Leu Ile Xaa Gly Cys Pro Ile Lys Phe Asn Val Ser Gly Asn
 195 200 205
 Lys Gly Gln Lys Asn Asn Ile Glu Leu Ile Ala Lys Gln Arg Ser Phe
 210 215 220
 Ile Asp Tyr Trp Ala Lys Tyr
 225 230

(2) INFORMATION FOR SEQ ID NO: 177:

00765272 012201

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 550 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 177:

TTACCGCGTT CATCAAGATG TCAAACAAGT CATGACCTAT CAACCCATGG TCGGAGAAAT	60
ATTGAGTGAA CAAGACACCC CAGCAAACGA AGAGCTTGTG CTGCTATGA TTTATACTGA	120
AACAAAAGGA AAAGAAGGCG ATGTTATGCA GTCTAGTGAG TCTGCAAGTG GTTCCACCAA	180
CACCATCAAT GATAATGCTT CTAGCATTCG GCAAGGCATT CAAACTCTGA CAGGCAATCT	240
CTATCTGGCG CAGAAGAAGG GGGTAGATAT CTGGACAGCT GTTCAAGCCT ATAATTTTGG	300
ACCTGCCTAT ATCGATTTTA TCGCCCAAAA TGGCAAGGAA AATACCCTGG CTCTAGCCAA	360
ACAGTACTCT CGTGAGACTG TTGCCCCCTT GCTTGTAAT AGGACTGGAA AGACTTATAG	420
TTATATTAC CCCATTTCAC TTTTTCACGG TGCTGAACTC TATGTAAATG GAGGAAACTA	480
TTATTATTCT AGACAGGTAC GACTTAACCT TTACATCATC AAATGTTTCA CTCTCTTTTC	540
AACATCTGGC	550

(2) INFORMATION FOR SEQ ID NO:178:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 183 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

Tyr Arg Val His Gln Asp Val Lys Gln Val Met Thr Tyr Gln Pro Met	
1 5 10 15	
Val Arg Glu Ile Leu Ser Glu Gln Asp Thr Pro Ala Asn Glu Glu Leu	
20 25 30	
Val Leu Ala Met Ile Tyr Thr Glu Thr Lys Gly Lys Glu Gly Asp Val	
35 40 45	
Met Gln Ser Ser Glu Ser Ala Ser Gly Ser Thr Asn Thr Ile Asn Asp	
50 55 60	
Asn Ala Ser Ser Ile Arg Gln Gly Ile Gln Thr Leu Thr Gly Asn Leu	
65 70 75 80	
Tyr Leu Ala Gln Lys Lys Gly Val Asp Ile Trp Thr Ala Val Gln Ala	
85 90 95	
Tyr Asn Phe Gly Pro Ala Tyr Ile Asp Phe Ile Ala Gln Asn Gly Lys	

	100		105		110
Glu Asn Thr Leu Ala Leu Ala Lys Gln Tyr Ser Arg Glu Thr Val Ala					
115		120		125	
Pro Leu Leu Gly Asn Arg Thr Gly Lys Thr Tyr Ser Tyr Ile His Pro					
130		135		140	
Ile Ser Ile Phe His Gly Ala Glu Leu Tyr Val Asn Gly Gly Asn Tyr					
145		150		155	160
Tyr Tyr Ser Arg Gln Val Arg Leu Asn Leu Tyr Ile Ile Lys Cys Phe					
	165		170		175
Thr Leu Phe Ser Thr Ser Gly					
180					

(2) INFORMATION FOR SEQ ID NO: 179:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 334 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179:

GTGGATGGGC TTAACTATC TTCGTATTCG CCGTGCGGCT AAAATTGTGG ACAATGAGGA	50
GTTTGAAGCC TTGATTGTA CGGGTCAATT GATTGATTG CGCGACCCAG CAGAATCCCA	120
CAGAAAACAT ATCCTTGGTG CACGCAATAT TCCTTCAAGT CAGTTGAAAA CTAGTCTTGC	180
AGCCCTTCGT AAAGATAAC CTGTCCTTCT CTACGAAAC CAACGTGCGC AACGAGTTAC	240
AAATGCAGCT CTTTACTTGA AAAACAAGG TTTTCTGAG ATTTATATCC TTTCTTATGG	300
CTTGGATTCT TGGAAAGGA AAGTGAAGAC TAGC	334

(2) INFORMATION FOR SEQ ID NO:180:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 111 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

Trp Met Gly Phe Asn Tyr Leu Arg Ile Arg Arg Ala Ala Lys Ile Val			
1	5	10	15
Asp Asn Glu Glu Phe Glu Ala Leu Ile Arg Thr Gly Gln Leu Ile Asp			
20	25	30	
Leu Arg Asp Pro Ala Glu Phe His Arg Lys His Ile Leu Gly Ala Arg			
35	40	45	

Asn Ile Pro Ser Ser Gln Leu Lys Thr Ser Leu Ala Ala Leu Arg Lys
 50 55 60
 Asp Lys Pro Val Leu Leu Tyr Glu Asn Gln Arg Ala Gln Arg Val Thr
 65 70 75 80
 Asn Ala Ala Leu Tyr Leu Lys Lys Gln Gly Phe Ser Glu Ile Tyr Ile
 85 90 95
 Leu Ser Tyr Gly Leu Asp Ser Trp Lys Gly Lys Val Lys Thr Ser
 100 105 110

(2) INFORMATION FOR SEQ ID NO: 181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1342 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181:

ACTAAACACG CATCGTTCGC AGGAAAATAA GGACAATAAT CGTGCTCTTT ATGTGGATGG 60
 CAGCCAGTCA AGTCAGAAA GTGAAAACCT GACACCAGAC CAGGTTAGCC AGAAAGAAGG 120
 AATTCAGGCT GAGCAAATTG TAATCAAAAT TACAGATCAG GGCTATGTAA CGTCACACGG 180
 TGACCACTAT CATTACTATA ATGGGAAAGT TCCTTATGAT GCCCTCTTTA GTGAGAACT 240
 CTTGATGAAG GATCCAAACT ATCAACTTAA AGACGCTGAT ATTGTCAATG AAGTCAAGGG 300
 TGGTTATATC ATCAAGGTCG ATGGAAAATA TTATGTCTAC CTGAAAGATG CAGCTCATGC 360
 TGATAATGTT CGAACTAAG ATGAAATCAA TCGTCAAAAA CAAGAACATG TCAAAGATAA 420
 TGAGAAGGTT AACTCTAATG TTGCTGTAGC AAGGTCACAG GGACGATATA CGACAAATGA 480
 TGGTTATGTC TTTAATCCAG CTGATATTAT CGAAGATACG GGTAATGCTT ATATCGTTCC 540
 TCATGGAGGT CACTATCACT ACATATCCCA AAGCGATTTA TCTGCTAGTG AATTAGCAGC 600
 AGCTAAAGCA CATCTGGCTG GAAAAATAT GCAACCGAGT CAGTTAAGCT ATTCTTCAAC 660
 AGCTAGTGAC AATAACACGC AATCTGTAGC AAAAGGATCA ACTAGCAAGC CAGCAAATAA 720
 ATCTGAAAAA CTCAGAGATC TTTTGAAGGA ACTCTATGAT TCACCTAGCG CCCAACGTTA 780
 CAGTGAATCA GATGGCCTGG TCTTTGACCC TGCTAAGATT ATCAGTCGTA CACCAAAATGG 840
 AGTTCGCATT CCGCATGGCG ACCATTACCA CTTTATTCTT TACAGCAAGC TTTCTGCCTT 900
 AGAAGAAAAG ATTGCCAGAA TGGTGCCTAT CAGTGGAAC TGGTCTACAG TTTCTACAAA 960
 TGCAAAACCT AATGAAGTAG TGTCTAGTCT AGGCAGTCTT TCAAGCAATC CTTCTTCTTT 1020
 AACGACAAGT AAGGAGCTCT CTTCAGCATC TGATGGTTAT ATTTTAAATC CAAAAGATAT 1080
 CGTTGAAGAA ACGGCTACAG CTTTATATTGT AAGACATGGT GATCATTTC CATTACATTC 1140
 AAAATCAAAT CAAATTGGGC AACCGACTCT TCCAAACAAT AGTCTAGCAA CACCTTCTCC 1200

ATCTCTTCCA ATCAATCCAG GAACTTCACA TGAGAAACAT GAAGAAGATG GATACGGATT 1260
 TGATGCTAAT CGTATTATCG CTGAAGATGA ATCAGGTTTT GTCATGAGTC ACGGAGACCA 1320
 CAATCATTAT TTCTTCAAGA AG 1342

(2) INFORMATION FOR SEQ ID NO:182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

Leu Asn Gln His Arg Ser Gln Glu Asn Lys Asp Asn Asn Arg Val Ser 1 5 10 15
 Tyr Val Asp Gly Ser Gln Ser Ser Gln Lys Ser Glu Asn Leu Thr Pro 20 25 30
 Asp Gln Val Ser Gln Lys Glu Gly Ile Gln Ala Glu Gln Ile Val Ile 35 40 45
 Lys Ile Thr Asp Gln Gly Tyr Val Thr Ser His Gly Asp His Tyr His 50 55 60
 Tyr Tyr Asn Gly Lys Val Pro Tyr Asp Ala Leu Phe Ser Glu Glu Leu 65 70 75 80
 Leu Met Lys Asp Pro Asn Tyr Gln Leu Lys Asp Ala Asp Ile Val Asn 85 90 95
 Glu Val Lys Gly Gly Tyr Ile Ile Lys Val Asp Gly Lys Tyr Tyr Val 100 105 110
 Tyr Leu Lys Asp Ala Ala His Ala Asp Asn Val Arg Thr Lys Asp Glu 115 120
 Ile Asn Arg Gln Lys Gln Glu His Val Lys Asp Asn Glu Lys Val Asn 130 135 140
 Ser Asn Val Ala Val Ala Arg Ser Gln Gly Arg Tyr Thr Thr Asn Asp 145 150 155 160
 Gly Tyr Val Phe Asn Pro Ala Asp Ile Ile Glu Asp Thr Gly Asn Ala 165 170 175
 Tyr Ile Val Pro His Gly Gly His Tyr His Tyr Ile Pro Lys Ser Asp 180 185 190
 Leu Ser Ala Ser Glu Leu Ala Ala Ala Lys Ala His Leu Ala Gly Lys 195 200 205
 Asn Met Gln Pro Ser Gln Leu Ser Tyr Ser Ser Thr Ala Ser Asp Asn 210 215 220
 Asn Thr Gln Ser Val Ala Lys Gly Ser Thr Ser Lys Pro Ala Asn Lys

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225 230 235 240
 Ser Glu Asn Leu Gln Ser Leu Leu Lys Glu Leu Tyr Asp Ser Pro Ser
 245 250 255
 Ala Gln Arg Tyr Ser Glu Ser Asp Gly Leu Val Phe Asp Pro Ala Lys
 260 265 270
 Ile Ile Ser Arg Thr Pro Asn Gly Val Ala Ile Pro His Gly Asp His
 275 280 285
 Tyr His Phe Ile Pro Tyr Ser Lys Leu Ser Ala Leu Glu Glu Lys Ile
 290 295 300
 Ala Arg Met Val Pro Ile Ser Gly Thr Gly Ser Thr Val Ser Thr Asn
 305 310 315 320
 Ala Lys Pro Asn Glu Val Val Ser Ser Leu Gly Ser Leu Ser Ser Asn
 325 330 335
 Pro Ser Ser Leu Thr Thr Ser Lys Glu Leu Ser Ser Ala Ser Asp Gly
 340 345 350
 Tyr Ile Phe Asn Pro Lys Asp Ile Val Glu Glu Thr Ala Thr Ala Tyr
 355 360 365
 Ile Val Arg His Gly Asp His Phe His Tyr Ile Pro Lys Ser Asn Gln
 370 375 380
 Ile Gly Gln Pro Thr Leu Pro Asn Asn Ser Leu Ala Thr Pro Ser Pro
 385 390 395 400
 Ser Leu Pro Ile Asn Pro Gly Thr Ser His Glu Lys His Glu Glu Asp
 405 410 415
 Gly Tyr Gly Phe Asp Ala Asn Arg Ile Ala Glu Asp Glu Ser Gly
 420 425 430
 Phe Val Met Ser His Gly Asp His Asn His Tyr Phe Phe Lys Lys
 435 440 445

(2) INFORMATION FOR SEQ ID NO: 183:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 934 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183:

TGACTACCTT GAAATCCAC TTACAGCTA TCTGGTGA TTCAACACTA AAGTCTTC	60
AACTCCAATG ATGAACATCA TCAACGGTGG TTCTACTCT GACGCTCCAA TCGCTTCCA	120
AGAGTTCATG ATCTTGCCAG TTGGTGCGCC AACATTTAAA GAAGCCCTTC GTTACGGTGC	180
TGAAATCTTC CACGCTCTTA AGAAAACTCT TAAATCAGCT GGTTTGAAAA CTGCCGTAGG	240
TGACGAAGGT GGATTCGCTC CTCGTTTCGA AGGAAC TGAA GATGTGTTG AAATATCTCT	300

TGCTGCGATT GAAGCTGCTG GATATGTACC AGGTAAAGAC GTATTTATCG GATTTGACTG 360
 TGCTTCATCA GAATTCTACG ATAAAGAACG TAAAGTTTAC GACTACACTA AATTTGAAGG 420
 TGAAGGTGCT GCTGTTCTGA CATCTGCAGA ACAAATCGAC TACCTTGAAG AATTGGTTAA 480
 CAAATACCCA ATCATCTACT TTGAAGATGG TATGGATGAA AACGACTGGG ATGGTTGSAA 540
 AGCTCTTACT GAACGCTCTG GTAAGAAAAGT ACAACTTGTT GGTGACGACT TCTTCGTAAC 600
 AAACACTGAC TACCTTGCAC GTGGTATCCA AGAAGGTGCT GCTAACTCAA TCCTTATCAA 660
 AGTTAACCAA ATCGGTACTC TTAAGTAAAC TTTTGAAGCT ATCGAAATGG CTAAAGAAGC 720
 TGGTTACACT GCTGTTGTAT CACACCGTTC AGGTGAAACT GAAGATTCAA CAATCGCTGA 780
 TATTGCAGTT GCAACTAACG CAGGACAAAT CAAGACTGGT TCACTTTCAC GTACAGACCG 840
 CATCGCTAAA TACAACCAAT TGCTTCGTAT CGAAGACCAA CTTGGTGAAG TAGCTGAATA 900
 TCGTGGATTG AAATCATCTT ACAACCTTAA AAAA 934

(2) INFORMATION FOR SEQ ID NO:184:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 311 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

Asp Tyr Leu Glu Ile Pro Leu Tyr Ser Tyr Leu Gly Gly Phe Asn Thr
 1 5 10 15
 Lys Val Leu Pro Thr Pro Met Met Asn Ile Ile Asn Gly Gly Ser His
 20 25 30
 Ser Asp Ala Pro Ile Ala Phe Gln Glu Phe Met Ile Leu Pro Val Gly
 35 40 45
 Ala Pro Thr Phe Lys Glu Ala Leu Arg Tyr Gly Ala Glu Ile Phe His
 50 55 60
 Ala Leu Lys Lys Ile Leu Lys Ser Arg Gly Leu Glu Thr Ala Val Gly
 65 70 75 80
 Asp Glu Gly Gly Phe Ala Pro Arg Phe Glu Gly Thr Glu Asp Gly Val
 85 90 95
 Glu Thr Ile Leu Ala Ala Ile Glu Ala Ala Gly Tyr Val Pro Gly Lys
 100 105 110
 Asp Val Phe Ile Gly Phe Asp Cys Ala Ser Ser Glu Phe Tyr Asp Lys
 115 120 125
 Glu Arg Lys Val Tyr Asp Tyr Thr Lys Phe Glu Gly Glu Gly Ala Ala
 130 135 140
 Val Arg Thr Ser Ala Glu Gln Ile Asp Tyr Leu Glu Glu Leu Val Asn

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145 150 155 160

Lys Tyr Pro Ile Ile Thr Ile Glu Asp Gly Met Asp Glu Asn Asp Trp
165 170 175

Asp Gly Trp Lys Ala Leu Thr Glu Arg Leu Gly Lys Lys Val Gln Leu
180 185 190

Val Gly Asp Asp Phe Phe Val Thr Asn Thr Asp Tyr Leu Ala Arg Gly
195 200 205

Ile Gln Glu Gly Ala Ala Asn Ser Ile Leu Ile Lys Val Asn Gln Ile
210 215 220

Gly Thr Leu Thr Glu Thr Phe Glu Ala Ile Glu Met Ala Lys Glu Ala
225 230 235 240

Gly Tyr Thr Ala Val Val Ser His Arg Ser Gly Glu Thr Glu Asp Ser
245 250 255

Thr Ile Ala Asp Ile Ala Val Ala Thr Asn Ala Gly Gln Ile Lys Thr
260 265 270

Gly Ser Leu Ser Arg Thr Asp Arg Ile Ala Lys Tyr Asn Gln Leu Leu
275 280 285

Arg Ile Glu Asp Gln Leu Gly Glu Val Ala Glu Tyr Arg Gly Leu Lys
290 295 300

Ser Phe Tyr Asn Leu Lys Lys
305 310

(2) INFORMATION FOR SEQ ID NO: 185:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 541 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 185:

TCGTAICTTT TTTTGGAGCA ATGTTGCGCT AGAAGGACAT TCCATGGATC CGACCCTAGC	60
GGATGGCGAA ATTCTCTTCG TTGTAAACAA CCTTCTATT GACCGTTTTG ATATCGTGGT	120
GGCCCCAGAG GAAGATGSCA ATAAGGACAT CGTCAAGCGC GTGATTGGAA TGCCCTGGCGA	180
CACCATTCGT TACGAAAATG ATAACTCTA CATCAATGAC AAAGAAACGG ACGAGCCTTA	240
TCTAGCAGAC TATATCAAAC GCTTCAAGGA TGACAAACTC CAAAGCACTT ACTCAGGCAA	300
GGGCTTTGAA GGAATAAAG GAACTTTCTT TAGAAGTATC GCTCAAAAAG CTCAAGCCTT	360
CACAGTTGAT GTCAACTACA ACACCAACTT TAGCTTTACT GTTCCAGAAG GAGAATACCT	420
TCTCCTCGGA GATGACCGCT TGGTTTCGAG CGACAGCCGC CACGTAGGTA CCTTCAAAGC	480
AAAAGATATC ACAGGGGAAG CTAATTTCCG CTTATGGCCA ATCACCCTGA TCGGAACATT	540
T	541

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(2) INFORMATION FOR SEQ ID NO:186:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 180 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

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Arg Ile Phe Phe Trp Ser Asn Val Arg Val Glu Gly His Ser Met Asp
1           5           10           15

Pro Thr Leu Ala Asp Gly Glu Ile Leu Phe Val Val Lys His Leu Pro
20          25          30

Ile Asp Arg Phe Asp Ile Val Val Ala His Glu Glu Asp Gly Asn Lys
35          40          45

Asp Ile Val Lys Arg Val Ile Gly Met Pro Gly Asp Thr Ile Arg Tyr
50          55          60

Glu Asn Asp Lys Leu Tyr Ile Asn Asp Lys Glu Thr Asp Glu Pro Tyr
65          70          75          80

Leu Ala Asp Tyr Ile Lys Arg Phe Lys Asp Asp Lys Leu Gln Ser Thr
85          90          95

Tyr Ser Gly Lys Gly Phe Glu Gly Asn Lys Gly Thr Phe Phe Arg Ser
100         105         110

Ile Ala Gln Lys Ala Gln Ala Phe Thr Val Asp Val Asn Tyr Asn Thr
115         120         125

Asn Phe Ser Phe Thr Val Pro Glu Gly Glu Tyr Leu Leu Leu Gly Asp
130         135         140

Asp Arg Leu Val Ser Ser Asp Ser Arg His Val Gly Thr Phe Lys Ala
145         150         155         160

Lys Asp Ile Thr Gly Glu Ala Lys Phe Arg Leu Trp Pro Ile Thr Arg
165         170         175

Ile Gly Thr Phe
180

```

(2) INFORMATION FOR SEQ ID NO: 187:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 187:

GGACTCTCTC AAAGATGTGA AAGCAATGC TAGCGACAGC AAGCCTGCAC AGGACAAGAA

GGATGCAAAA CAAGGAACGG AAGATAGTAA GGATTCAGAT AAGATGACTG AAACAAATC 120
 AGTTCCGGCA GGAGTGATTG TGGTCAGTCT ACTTGCCCTC CTAGGCGTGA TTGCCTTCTG 180
 GCTGATTGCG CGTAAGAAAG AGTCAGAAAT CCAGCAATTA AGCACGGAAT TGATCAAGGT 240
 TCTAGGACAG CTAGATGCAg AAAAAAGCGGA TAAAAAAGTC CTTGCCAAG CCCAAAACCT 300
 TCTCCAAGAA ACCCTTGATT TCGTGAAAGA AGAAAATGGC TCAGCAGAGA CAGAAACTAA 360
 ACTAGTAGAG GAGCTTAAAG CAATCCTTGA CAAACTCAAG 400

(2) INFORMATION FOR SEQ ID NO:188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

Asp Ser Leu Lys Asp Val Lys Ala Asn Ala Ser Asp Ser Lys Pro Ala
 1 5 10 15
 Gln Asp Lys Lys Asp Ala Lys Gln Gly Thr Glu Asp Ser Lys Asp Ser
 20 25 30
 Asp Lys Met Thr Glu Thr Asn Ser Val Pro Ala Gly Val Ile Val Val
 35 40 45
 Ser Leu Leu Ala Leu Leu Gly Val Ile Ala Phe Trp Leu Ile Arg Arg
 50 55 60
 Lys Lys Glu Ser Glu Ile Gln Gln Leu Ser Thr Glu Leu Ile Lys Val
 65 70 75 80
 Leu Gly Gln Leu Asp Ala Glu Lys Ala Asp Lys Lys Val Leu Ala Lys
 85 90 95
 Ala Gln Asn Leu Leu Gln Glu Thr Leu Asp Phe Val Lys Glu Glu Asn
 100 105 110
 Gly Ser Ala Glu Thr Glu Thr Lys Leu Val Glu Glu Leu Lys Ala Ile
 115 120 125
 Leu Asp Lys Leu Lys
 130

(2) INFORMATION FOR SEQ ID NO: 189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1201 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 189:

CAAGAAATCC TATCATCTCT TCCAGAAGCA AACAGAGACG AGGGGAATTC AGACTCAGTT 60
 GATTGAAGAA TCGCTTAGTC AGCAGACTAT AATCCAGTCC TTCATGCTC AAACAGAATT 120
 TATCCAAAGA TTGCGTGAGG CTCATGACAA CTACTCAGGC TATTCTCAGT CAGCCATCTT 180
 TTATTCTTCA ACGGTCAATC CTTGACTCG CTTTGTAAT GCACCTATT ATGCCCTTTT 240
 AGCTGGAGTA GGAGCTTATC GTATCATGAT GGGTTCAGCC TTGACCGTCG GTCGTTTAGT 300
 GACTTTTTTG AACTATGTT AGCAATACAC CAAGCCCTTT AACGATATT CTTCAGTGCT 360
 AGCTGAGTTG CAAAGTGCTC TGGCTTGCGT AGAGCGTATC TATGGAGTCT TAGATAGCCC 420
 TGAAGTGGCT GAAACAGGTA AGGAAGTCTT GACGACCACT GACCAAGTTA AGGGAGCTAT 480
 TTCCTTTAAA CATGCTCTTT TTGGCTACCA TCCTGAAAAA ATTTTGATTA AGGACTTGTC 540
 TATCGATATT CCAGCTGGTA GTAAGGTAGC CATCGTTGGT CCGACAGGTG CTGGAAAAATC 600
 AACTCTTATC AATCTCCTTA TGCCTTTTTA TCCCATAGC TCGGGAGATA TCTTGCTGGA 660
 TGGGCAATCC ATTTATGATT ATACACGAGT ATCATTGAGA CAGCAGTTTG GTATGGTGCT 720
 TCAAGAAACC TGGCTCACAC AAGGGACCAT TCATGATAAT ATTGCCTTTG GCAATCCTGA 780
 AGCCAGTCGA GAGCAAGTAA TTGCTGCTGC CAAAGCAGCT AATGCAGACT TTTTCATCCA 840
 ACAGTTGCCA CAGGATACG ATACCAAGTT GGAATGCT GGAGAATCTC TCTCTGTCGG 900
 CCAAGCTCAG CTCTTGACCA TAGCCCGAGT CTTCTGCGT ATTCCAAGA TTCTTATCTT 960
 AGACGAGGCA ACTTCTTCCA TTGATACAG GACAGAAGTG CTGGTACAGG ATGCCTTTGC 1020
 AAAACTCATG AAGGGCCGCA CAAGTTTCAT CATTGCTCAC CGTTTGICAA CCATTCAGGA 1080
 TGC GGATTTA ATCTTGCTCT TAGTAGATGG TGATATTGTT GAATATGGTA ACCATCAAGA 1140
 ACTCATGGAT AGAAAGGGTA AGTATTACCA AATGCAAAAA GCTGCGGCTT TTAGTCTGA 1200
 A 1201

(2) INFORMATION FOR SEQ ID NO:190:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

Lys Lys Ser Tyr His Leu Phe Gln Lys Gln Thr Glu Thr Arg Gly Ile
 1 5 10 15
 Gln Thr Gln Leu Ile Glu Glu Ser Leu Ser Gln Gln Thr Ile Ile Gln
 20 25 30

Ser Phe Asn Ala Gln Thr Glu Phe Ile Gln Arg Leu Arg Glu Ala His
 35 40 45
 Asp Asn Tyr Ser Gly Tyr Ser Gln Ser Ala Ile Phe Tyr Ser Ser Thr
 50 55 60
 Val Asn Pro Ser Thr Arg Phe Val Asn Ala Leu Ile Tyr Ala Leu Leu
 65 70 75 80
 Ala Gly Val Gly Ala Tyr Arg Ile Met Met Gly Ser Ala Leu Thr Val
 85 90 95
 Gly Arg Leu Val Thr Phe Leu Asn Tyr Val Gln Gln Tyr Thr Lys Pro
 100 105 110
 Phe Asn Asp Ile Ser Ser Val Leu Ala Glu Leu Gln Ser Ala Leu Ala
 115 120 125
 Cys Val Glu Arg Ile Tyr Gly Val Leu Asp Ser Pro Glu Val Ala Glu
 130 135 140
 Thr Gly Lys Glu Val Leu Thr Thr Ser Asp Gln Val Lys Gly Ala Ile
 145 150 155 160
 Ser Phe Lys His Val Ser Phe Gly Tyr His Pro Glu Lys Ile Leu Ile
 165 170 175
 Lys Asp Leu Ser Ile Asp Ile Pro Ala Gly Ser Lys Val Ala Ile Val
 180 185 190
 Gly Pro Thr Gly Ala Gly Lys Ser Thr Leu Ile Asn Leu Leu Met Arg
 195 200 205
 Phe Tyr Pro Ile Ser Ser Gly Asp Ile Leu Leu Asp Gly Gln Ser Ile
 210 215 220
 Tyr Asp Tyr Thr Arg Val Ser Leu Arg Gln Gln Phe Gly Met Val Leu
 225 230 235 240
 Gln Glu Thr Trp Leu Thr Gln Gly Thr Ile His Asp Asn Ile Ala Phe
 245 250 255
 Gly Asn Pro Glu Ala Ser Arg Glu Gln Val Ile Ala Ala Lys Ala
 260 265 270
 Ala Asn Ala Asp Phe Phe Ile Gln Gln Leu Pro Gln Gly Tyr Asp Thr
 275 280 285
 Lys Leu Glu Asn Ala Gly Glu Ser Leu Ser Val Gly Gln Ala Gln Leu
 290 295 300
 Leu Thr Ile Ala Arg Val Phe Leu Ala Ile Pro Lys Ile Leu Ile Leu
 305 310 315 320
 Asp Glu Ala Thr Ser Ser Ile Asp Thr Arg Thr Glu Val Leu Val Gln
 325 330 335
 Asp Ala Phe Ala Lys Leu Met Lys Gly Arg Thr Ser Phe Ile Ile Ala
 340 345 350
 His Arg Leu Ser Thr Ile Gln Asp Ala Asp Leu Ile Leu Val Leu Val
 355 360 365

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Asp Gly Asp Ile Val Glu Tyr Gly Asn His Gln Glu Leu Met Asp Arg
370 375 380

Lys Gly Lys Tyr Tyr Gln Met Gln Lys Ala Ala Ala Phe Ser Ser Glu
385 390 395 400

(2) INFORMATION FOR SEQ ID NO: 191:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1033 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 191:

ACGAAATGCA GGGCAGACAG ATGCCTCGCA AATTGAAAAG GCGGCAGTTA GCCAAGGAGG 60
AAAAGCAGTG AAAAAACAG AAATTAGTAA AGACGCAGAC TTGCACGAAA TTTATCTAGC 120
TGGAGGTTGT TTCTGGGGAG TGGAGGAATA TTTCTCAGCT GTTCCCGGGG TGACGGGATGC 180
CGTTTCAGGC TATGCAAAATG GTAGAGGAGA AACAAACCAAG TACGAATTGA TTAACCAAC 240
AGGTCATGCA GAAACCGTCC ATGTCACCTA TGATGCCAAG CAAATTTCTC TCAAGGAAAT 300
CCTGCTTCAC TATTTCCGCA TTATCAATCC AACCAGCAA AATAACAAG GAAATGATGT 360
GGGGACCCAG TACCGTACTG GTGTTTATTA CACAGATGAC AAGGATTTGG AAGTGATTAA 420
CCAAGTCTTT GATGAGGTGG CTAAGAAATA CGATCAACCT CTAGCAGTTG AAAAGGAAAA 480
CTTGAAGAAT TTTGTGGTGG CTGAGGATTA CCATCAAGAC TATCTCAAGA AAAATCCAAA 540
TGGCTACTGC CATATCAATG TTAATCAGGC GGCCTATCCT GTCATTGATG CCAGCAAATA 600
TCCAAAACCA AGTGATGAGG AATTGAAAAA GACCCGTGCA CTTGAGGAGT ATGCAGTTAC 660
CCAGGAAAT CAACACGAAC GAGCTTTCTC AAACCGTTAC TGGGATAAAT TTGAATCCGG 720
TATCTATGTG GATATAGCAA CTGGGGAACC TCTCTTTTCA TCAAAGACA AATTGTAGTC 780
TGGTTGTGGC TGGCCTAGTT TTACCCAACC CATCAGTCCA GATGTTGTCA CCTACAAGGA 840
AGATAAGTCC TACAATATGA CGCGTATGGA AGTGCGGAGC CGAGTAGGAG ATTCTCACCT 900
TGGCATGTCT TTTACGGATG GTCCACAGGA CAAGGGCGGC TTACGTTACT GTATCAATAG 960
CCTCTCTACT CGCTTTATTC CCAAGACCA AATGGAAGAA AAAGGCTACG CTTATTTACT 1020
AGATTATGTT GAT 1033

(2) INFORMATION FOR SEQ ID NO:192:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 344 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

Arg Asn Ala Gly Gln Thr Asp Ala Ser Gln Ile Glu Lys Ala Ala Val
 1 5 10 15
 Ser Gln Gly Gly Lys Ala Val Lys Lys Thr Glu Ile Ser Lys Asp Ala
 20 25 30
 Asp Leu His Glu Ile Tyr Leu Ala Gly Gly Cys Phe Trp Gly Val Glu
 35 40 45
 Glu Tyr Phe Ser Arg Val Pro Gly Val Thr Asp Ala Val Ser Gly Tyr
 50 55 60
 Ala Asn Gly Arg Gly Glu Thr Thr Lys Tyr Glu Leu Ile Asn Gln Thr
 65 70 75 80
 Gly His Ala Glu Thr Val His Val Thr Tyr Asp Ala Lys Gln Ile Ser
 85 90 95
 Leu Lys Glu Ile Leu Leu His Tyr Phe Arg Ile Ile Asn Pro Thr Ser
 100 105 110
 Lys Asn Lys Gln Gly Asn Asp Val Gly Thr Gln Tyr Arg Thr Gly Val
 115 120 125
 Tyr Tyr Thr Asp Asp Lys Asp Leu Glu Val Ile Asn Gln Val Phe Asp
 130 135 140
 Glu Val Ala Lys Lys Tyr Asp Gln Pro Leu Ala Val Glu Lys Glu Asn
 145 150 155 160
 Leu Lys Asn Phe Val Val Ala Glu Asp Tyr His Gln Asp Tyr Leu Lys
 165 170 175
 Lys Asn Pro Asn Gly Tyr Cys His Ile Asn Val Asn Gln Ala Ala Tyr
 180 185 190
 Pro Val Ile Asp Ala Ser Lys Tyr Pro Lys Pro Ser Asp Glu Glu Leu
 195 200 205
 Lys Lys Thr Leu Ser Pro Glu Glu Tyr Ala Val Thr Gln Glu Asn Gln
 210 215 220
 Thr Glu Arg Ala Phe Ser Asn Arg Tyr Trp Asp Lys Phe Glu Ser Gly
 225 230 235 240
 Ile Tyr Val Asp Ile Ala Thr Gly Glu Pro Leu Phe Ser Ser Lys Asp
 245 250 255
 Lys Phe Glu Ser Gly Cys Gly Trp Pro Ser Phe Thr Gln Pro Ile Ser
 260 265 270
 Pro Asp Val Val Thr Tyr Lys Glu Asp Lys Ser Tyr Asn Met Thr Arg
 275 280 285
 Met Glu Val Arg Ser Arg Val Gly Asp Ser His Leu Gly His Val Phe
 290 295 300
 Thr Asp Gly Pro Gln Asp Lys Gly Gly Leu Arg Tyr Cys Ile Asn Ser
 305 310 315 320

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Leu Ser Ile Arg Phe Ile Pro Lys Asp Gln Met Glu Glu Lys Gly Tyr
 325 330 335

Ala Tyr Leu Leu Asp Tyr Val Asp
 340

(2) INFORMATION FOR SEQ ID NO: 193:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 396 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 193:

TGTATAGTTT TTAGCGCTTG TTCTTCTAAT TCTGNTAAAA ATGAAGAAAA TACTTCTAAA	60
GAGCATGCGC CTGATAAAT AGTTTTAGAT CATGCTTTCG GTCAACTAT ATTAGATAAA	120
AAACCTGAAA GAGTIGCAAC TATTGCTTGG GGAATCATG ATGTAGCATT AGCTTTAGGA	180
ATAGTTCCTG TTGGATTTTC AAAAGCAAAT TACGGGTGTA GTGCTGATAA AGGAGTTTAA	240
CCATGGACAG AAGAAAAAAT CAAAGAACTA AATGGTAAAG CTAACCTATT TGACGATTTG	300
GATGGACTTA ACTTTGAAGC AATATCAAAT TCTAAACCAG ATGTTATCTT AGCAGGTTAT	360
TCTGGTATAA CTAAGAAGA TTATGACACT CTATCA	396

(2) INFORMATION FOR SEQ ID NO:194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

Cys Ile Val Phe Ser Ala Cys Ser Ser Asn Ser Xaa Lys Asn Glu Glu	
1 5 10 15	
Asn Thr Ser Lys Glu His Ala Pro Asp Lys Ile Val Leu Asp His Ala	
20 25 30	
Phe Gly Gln Thr Ile Leu Asp Lys Lys Pro Glu Arg Val Ala Thr Ile	
35 40 45	
Ala Trp Gly Asn His Asp Val Ala Leu Ala Leu Gly Ile Val Pro Val	
50 55 60	
Gly Phe Ser Lys Ala Asn Tyr Gly Val Ser Ala Asp Lys Gly Val Leu	
65 70 75 80	
Pro Trp Thr Glu Glu Lys Ile Lys Glu Leu Asn Gly Lys Ala Asn Leu	
85 90 95	

09755272.01204

Phe Asp Asp Leu Asp Gly Leu Asn Phe Glu Ala Ile Ser Asn Ser Lys
 100 105 110

Pro Asp Val Ile Leu Ala Gly Tyr Ser Gly Ile Thr Lys Glu Asp Tyr
 115 120 125

Asp Thr Leu Ser
 130

(2) INFORMATION FOR SEQ ID NO: 195:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 844 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 195:

GTGTGTCGAG CATATTCCTGA AGCAAACCTA TCAAAATATA GAAATTATTT TAGTTGATGA	60
CGGTTCTACG GATAATTCTG GGGAAATTG TGATGCTTTT ATGATGCAAG ATAATCGTGT	120
GCGAGTATTG CATCAAGAAA ATAAGGGGGG GGCAGCACAA GCTAAAAATA TGGGGATTAG	180
TGTAGCTAAG GGAGAGTACA TCACGATTGT TGATTCAGAT GATATCGTAA AAGAAAAATAT	240
GATTGAAACT CTTTATCAGC AAGTCCAAGA AAAGGATGCA GATGTTGTTA TAGGGAATTA	300
CTATAATTAT GACGAAAGTG ACGGGAATTT TTATTTTAT GTACACGGGC AAGATTTTTG	360
CGTCGAAGAA TTAGCTATAC AAGAAATTAT GAACCGTCAA GCAGGAGATT GGAATTCAA	420
TAGCTCGGCC TTTATATTGC CGACATTTAA GTTGATTAAA AAAGAATTAT TCAATGAAGT	480
TCACTTTTCA AATGGTCGCC GCTTTGATGA TGAAGCAACT ATGCATCGCT TTTATCTTTT	540
AGCCTCTAAA ATCGTCTTTA TAAACGATAA TCTCTATCTG TATAGAAGAC GTTCAGGAAG	600
CATCATGAGA ACGGAATTTG ATCTTTCCTG GGCAAGAGAT ATTGTTGAAG TGTTTCTTAA	660
GAAAATATCG GATTGTGTCT TGGCTGGTTT GGATGTCTCC GTTCTGCGTA TTCGATTGT	720
CAATCTTTTA AAAGATTATA AGCAAACCTT AGAATACCAT CAATTACAG ATACTGAGGA	780
ATATAAGAT ATTGTGTTCA GATTAAAGTT GTTTTTTGAT GCAGAACAAA GAAATGGTAA	840
AAGT	844

(2) INFORMATION FOR SEQ ID NO:196:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 281 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

007015271.1.F0004

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

Cys Val Glu His Ile Leu Lys Gln Thr Tyr Gln Asn Ile Glu Ile Ile
 1 5 10 15
 Leu Val Asp Asp Gly Ser Thr Asp Asn Ser Gly Glu Ile Cys Asp Ala
 20 25 30
 Phe Met Met Gln Asp Asn Arg Val Arg Val Leu His Gln Glu Asn Lys
 35 40 45
 Gly Gly Ala Ala Gln Ala Lys Asn Met Gly Ile Ser Val Ala Lys Gly
 50 55 60
 Glu Tyr Ile Thr Ile Val Asp Ser Asp Asp Ile Val Lys Glu Asn Met
 65 70 75 80
 Ile Glu Thr Leu Tyr Gln Gln Val Gln Glu Lys Asp Ala Asp Val Val
 85 90 95
 Ile Gly Asn Tyr Tyr Asn Tyr Asp Glu Ser Asp Gly Asn Phe Tyr Phe
 100 105 110
 Tyr Val Thr Gly Gln Asp Phe Cys Val Glu Glu Leu Ala Ile Gln Glu
 115 120 125
 Ile Met Asn Arg Gln Ala Gly Asp Trp Lys Phe Asn Ser Ser Ala Phe
 130 135 140
 Ile Leu Pro Thr Phe Lys Leu Ile Lys Lys Glu Leu Phe Asn Glu Val
 145 150 155 160
 His Phe Ser Asn Gly Arg Arg Phe Asp Asp Glu Ala Thr Met His Arg
 165 170 175
 Phe Tyr Leu Leu Ala Ser Lys Ile Val Phe Ile Asn Asp Asn Leu Tyr
 180 185 190
 Leu Tyr Arg Arg Arg Ser Gly Ser Ile Met Arg Thr Glu Phe Asp Leu
 195 200 205
 Ser Trp Ala Arg Asp Ile Val Glu Val Phe Ser Lys Lys Ile Ser Asp
 210 215 220
 Cys Val Leu Ala Gly Leu Asp Val Ser Val Leu Arg Ile Arg Phe Val
 225 230 235 240
 Asn Leu Leu Lys Asp Tyr Lys Gln Thr Leu Glu Tyr His Gln Leu Thr
 245 250 255
 Asp Thr Glu Glu Tyr Lys Asp Ile Cys Phe Arg Leu Lys Leu Phe Phe
 260 265 270
 Asp Ala Glu Gln Arg Asn Gly Lys Ser
 275 280

(2) INFORMATION FOR SEQ ID NO: 197:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 811 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

09765272.0122004

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197:

GTGTTTGGAT AGCATTGAGA ATCAGACGTA TCAAAATTTT GAGTGTATAT TAATCAATGA 60
 TGGCTCTCCA GATCATTCAT CCAAATATG TGAAGAATTT GTAGAGAAAG ATTCTCGTTT 120
 CAAATATTTT GAGAAAGCAA ACGGCGGTCT TTCATCAGCT CGTACCTAG GTATTGAATG 180
 TTCGGGGGGG GCGTACATTA CTTTGTAGA CTCTGATGAT TGGTTGGAAC ATGATGCTTT 240
 AGACCGGATTA TATGTGCTT TGA AAAAAGGA AAACGCAGAT ATTAGTATCG GCGCTTATAA 300
 TTCTTATGAT GAAACACGCT ATGTGTATAT GACTTATGTT ACGGATCCAG ATGATTCTCT 360
 AGAAGTGATA GAAGGTAAG CAATTATGGA TAGGGAAGGT GTCAAGAAG TCAGAAATGG 420
 GAACTGGACT GTAGTGTCT TGAAGTTATT CAAGAGAGAG TTAACAAG ATTTACCATT 480
 TCCTATAGGA AAAATTGCAG AGGATACTTA CTGGACATGG AAGGTACTTC TAAGAGCTTC 540
 GAGGATAGTC TATTTGAATC GTTGTGTTA CTGTACCGT GTTGGTTTAT CTGATACCTT 600
 ATCGAATACA TGGAGTGAAA AGCGTATGTA TGATGAAAT GGGGCTAGGG AAGAAAAGAT 660
 AGCTATTTTA GCAAGTTCAG ACTATGACTT GACCAATCAT ATTTGATT ATAAAAATAG 720
 ATTACAAAGA GTGATAGCAA AATTAGAAGA ACAAATATG CAGTTCACAG AGATTACAG 780
 AAGAATGATG GAAAATTTGT CTTTACTTCC G 811

(2) INFORMATION FOR SEQ ID NO:198:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

Cys Leu Asp Ser Ile Gln Asn Gln Thr Tyr Gln Asn Phe Glu Cys Leu
 1 5 10 15
 Leu Ile Asn Asp Gly Ser Pro Asp His Ser Ser Lys Ile Cys Glu Glu
 20 25 30
 Phe Val Glu Lys Asp Ser Arg Phe Lys Tyr Phe Glu Lys Ala Asn Gly
 35 40 45
 Gly Leu Ser Ser Ala Arg Asn Leu Gly Ile Glu Cys Ser Gly Gly Ala
 50 55 60
 Tyr Ile Thr Phe Val Asp Ser Asp Asp Trp Leu Glu His Asp Ala Leu
 65 70 75 80
 Asp Arg Leu Tyr Gly Ala Leu Lys Lys Glu Asn Ala Asp Ile Ser Ile
 85 90 95

09765272-012201

Gly Arg Tyr Asn Ser Tyr Asp Glu Thr Arg Tyr Val Tyr Met Thr Tyr
 100 105 110
 Val Thr Asp Pro Asp Asp Ser Leu Glu Val Ile Glu Gly Lys Ala Ile
 115 120 125
 Met Asp Arg Glu Gly Val Glu Glu Val Arg Asn Gly Asn Trp Thr Val
 130 135 140
 Ala Val Leu Lys Leu Phe Lys Arg Glu Leu Leu Gln Asp Leu Pro Phe
 145 150 155 160
 Pro Ile Gly Lys Ile Ala Glu Asp Thr Tyr Trp Thr Trp Lys Val Leu
 165 170 175
 Leu Arg Ala Ser Arg Ile Val Tyr Leu Asn Arg Cys Val Tyr Trp Tyr
 180 185 190
 Arg Val Gly Leu Ser Asp Thr Leu Ser Asn Thr Trp Ser Glu Lys Arg
 195 200 205
 Met Tyr Asp Glu Ile Gly Ala Arg Glu Glu Lys Ile Ala Ile Leu Ala
 210 215 220
 Ser Ser Asp Tyr Asp Leu Thr Asn His Ile Leu Ile Tyr Lys Asn Arg
 225 230 235 240
 Leu Gln Arg Val Ile Ala Lys Leu Glu Glu Gln Asn Met Gln Phe Thr
 245 250 255
 Glu Ile Tyr Arg Arg Met Met Glu Lys Leu Ser Leu Leu Pro
 260 265 270

(2) INFORMATION FOR SEQ ID NO: 199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2023 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 199:

GTGCCTAGAT AGTATTATTA CTCAAACATA TAAAAATATT GAGATTGTTG TCGTTAATGA	60
TGGTTCTACG GATGCTTCAG GTGAAATTTG TAAAGAATTT TCAGAAATGG ATCACCAGAAT	120
TCTCTATATA GAACAAGAAA ATGCTGGTCT TTCTGCCGCA CGAAACACCG GTCTGAATAA	180
TATGTCGGGA AATTATGTGA CTTTGTGGA CTCGGATGAT TGGATTGAGC AAGATTATGT	240
AGAACTCTA TATAAAAAA TAGTAGAGTA TCAGGCTGAT ATTGCAGTTG GTAATTATTA	300
TTCTTTCAAC GAAAGTGAAG GAATGTTCTA CTTTCATATA TTGGAGACT CCTATTATGA	360
GAAAGTATAT GATAATGTTT CTATCTTTGA GAACTTGAT GAACTCAAG AAATGAAGAG	420
TTTTGCTTTG ATATCTGCTT GGGGTAAACT CTATAAGGCA AGATTGTTTG AGCAGTTGCG	480
CTTTGACATA GGTAATTAG GAGAAGATGG TTACCTCAAT CAAAAGGTAT ATTTATTATC	540

AGAAAAGGTA ATTTATTTAA ATAAAAGTCT TTATGCTTAT CGGATTAGAA AAGGTAGTTT 600
 ATCAAGAGTT TGGACAGAAA AGTGGATGCA CGCTTTAGTT GATGCTATGT CTGAACGTAT 660
 TACGCTACTA GCTAATATGG GTTATCCTCT AGAGAAACAC TTGGCAGTTT ATCGTCAGAT 720
 GTTGGAAGTC AGTCTCGCCA ACGGTCAAGC TAGTGGTTTA TCTGACACAG CAACGTATAA 780
 AGAGTTTGAA ATGAACAAA GGCTTTTAAA TCAGCTATCG AGACAAGAGG AAGTGAAAA 840
 GAAAGCCATT GTCCTCGCAG CAAACTATGG CTATGTAGAC CAAGTTTAA CGACAATCAA 900
 GTCTATTGTT TATCATAATC GTTCGATTCG TTTTATCTG ATTCATAGCG ATTTTCCAAA 960
 TGAATGGATT AAGCAATTAA ATAAGCGCTT AGAGAAGTTT GACTCAGAAA TTATTAATTG 1020
 TCGGGTAAGT TCTGAGCAAA TTTCATGTTA TAAATCGGAT ATTAGTTACA CAGTCTTTT 1080
 ACGCTATTTC ATAGCTGATT TCGTGCAAGA AGACAAGGCC CTCTACTTGG ACTGTGATCT 1140
 AGTGTGAACG AAAAATCTGG ATGACTTGTT TGCTACAGAC TTACAAGATT ATCCTTTGGC 1200
 TGCTGTAGAA GATTTTGGGG GCAGAGCTTA TTTTGTCAA GAAATCTTTA ATGCCGGTGT 1260
 TCTCTTGGTA AACATGCTT TTTGGAAAA AGAAGATATG ACCCAAAAT TAATTGATGT 1320
 AACCAATGAA TGGCATGATA AGGTGGATCA GGCAGATCAG AGCATCTTGA ATATGCTTTT 1380
 TGAACATAAA TGGTTGGAAT TGGACTTTGA TTATAATCAT ATTGTCATTC ATAAACAGTT 1440
 TGCTGATTAT CAATTGCCTG AGGGTCAGGA TTATCCTGCT ATTATTCATC ATCTTTCTCA 1500
 TCGGAAACCG TGGAAAGATT TGGCGGCCCA AACCTATCGT GAAGTTTGGT GGTACTATCA 1560
 TGGGCTTGAA TGGACAGAAT TGGGACAAAA CCATCATTTA CATCCATTAC AAAGATCTCA 1620
 CATCTATCCA ATAAAGGAAC CTTTCACTTG TCTAATCTAT ACTGCCTCAG ACCATATTGA 1680
 ACAAAATGAG ACATTGGTTC AATCCTTGCC TGATATTCAG TTAAAGATAG CAGCTAGAGT 1740
 AATAGTTAGT GATCGATTGG CTCAGATGAC AATTTATCCA AACGTGACTA TATTAAACGG 1800
 AATTCACTAT TTGGTAGATG TCGATAATGA ATTGGTAGAA ACCAGTCAAG TACTTTTAGA 1860
 TATTATCATC GCGGAAAAGA CAGAAGAAAT TCTCGATCAA TTTGCTAATC TTGGCAAGCC 1920
 TATCTTATCC TTTGAAAATA CTAACACCTA TGAAGTAGGT CAGGAGGCAT ATGCTGTTGA 1980
 CCAAGTTCAA GCAATGATTG AAAAATTGAG AGAAATAAGC AAA 2023

(2) INFORMATION FOR SEQ ID NO:200:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 674 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

09765272.012203

Cys Leu Asp Ser Ile Ile Thr Gln Thr Tyr Lys Asn Ile Glu Ile Val
 1 5 10 15
 Val Val Asn Asp Gly Ser Thr Asp Ala Ser Gly Glu Ile Cys Lys Glu
 20 25 30
 Phe Ser Glu Met Asp His Arg Ile Leu Tyr Ile Glu Gln Glu Asn Ala
 35 40 45
 Gly Leu Ser Ala Ala Arg Asn Thr Gly Leu Asn Asn Met Ser Gly Asn
 50 55 60
 Tyr Val Thr Phe Val Asp Ser Asp Asp Trp Ile Glu Gln Asp Tyr Val
 65 70 75 80
 Glu Thr Leu Tyr Lys Lys Ile Val Glu Tyr Gln Ala Asp Ile Ala Val
 85 90 95
 Gly Asn Tyr Tyr Ser Phe Asn Glu Ser Glu Gly Met Phe Tyr Phe His
 100 105 110
 Ile Leu Gly Asp Ser Tyr Tyr Glu Lys Val Tyr Asp Asn Val Ser Ile
 115 120 125
 Phe Glu Asn Leu Tyr Glu Thr Gln Glu Met Lys Ser Phe Ala Leu Ile
 130 135 140
 Ser Ala Trp Gly Lys Leu Tyr Lys Ala Arg Leu Phe Glu Gln Leu Arg
 145 150 155 160
 Phe Asp Ile Gly Lys Leu Gly Glu Asp Gly Tyr Leu Asn Gln Lys Val
 165 170 175
 Tyr Leu Leu Ser Glu Lys Val Ile Tyr Leu Asn Lys Ser Leu Tyr Ala
 180 185 190
 Tyr Arg Ile Arg Lys Gly Ser Leu Ser Arg Val Trp Thr Glu Lys Trp
 195 200 205
 Met His Ala Leu Val Asp Ala Met Ser Glu Arg Ile Thr Leu Leu Ala
 210 215 220
 Asn Met Gly Tyr Pro Leu Glu Lys His Leu Ala Val Tyr Arg Gln Met
 225 230 235 240
 Leu Glu Val Ser Leu Ala Asn Gly Gln Ala Ser Gly Leu Ser Asp Thr
 245 250 255
 Ala Thr Tyr Lys Glu Phe Glu Met Lys Gln Arg Leu Leu Asn Gln Leu
 260 265 270
 Ser Arg Gln Glu Glu Ser Glu Lys Lys Ala Ile Val Leu Ala Ala Asn
 275 280 285
 Tyr Gly Tyr Val Asp Gln Val Leu Thr Thr Ile Lys Ser Ile Cys Tyr
 290 295 300
 His Asn Arg Ser Ile Arg Phe Tyr Leu Ile His Ser Asp Phe Pro Asn
 305 310 315 320
 Glu Trp Ile Lys Gln Leu Asn Lys Arg Leu Glu Lys Phe Asp Ser Glu
 325 330 335

00765272-012004

Ile Ile Asn Cys Arg Val Thr Ser Glu Gln Ile Ser Cys Tyr Lys Ser
 340 345 350
 Asp Ile Ser Tyr Thr Val Phe Leu Arg Tyr Phe Ile Ala Asp Phe Val
 355 360 365
 Gln Glu Asp Lys Ala Leu Tyr Leu Asp Cys Asp Leu Val Val Thr Lys
 370 375 380
 Asn Leu Asp Asp Leu Phe Ala Thr Asp Leu Gln Asp Tyr Pro Leu Ala
 385 390 395 400
 Ala Val Arg Asp Phe Gly Gly Arg Ala Tyr Phe Gly Gln Glu Ile Phe
 405 410 415
 Asn Ala Gly Val Leu Leu Val Asn Asn Ala Phe Trp Lys Lys Glu Asn
 420 425 430
 Met Thr Gln Lys Leu Ile Asp Val Thr Asn Glu Trp His Asp Lys Val
 435 440 445
 Asp Gln Ala Asp Gln Ser Ile Leu Asn Met Leu Phe Glu His Lys Trp
 450 455 460
 Leu Glu Leu Asp Phe Asp Tyr Asn His Ile Val Ile His Lys Gln Phe
 465 470 475 480
 Ala Asp Tyr Gln Leu Pro Glu Gly Gln Asp Tyr Pro Ala Ile Ile His
 485 490 495
 Tyr Leu Ser His Arg Lys Pro Trp Lys Asp Leu Ala Ala Gln Thr Tyr
 500 505 510
 Arg Glu Val Trp Trp Tyr Tyr His Gly Leu Glu Trp Thr Glu Leu Gly
 515 520 525
 Gln Asn His His Leu His Pro Leu Gln Arg Ser His Ile Tyr Pro Ile
 530 535 540
 Lys Glu Pro Phe Thr Cys Leu Ile Tyr Thr Ala Ser Asp His Ile Glu
 545 550 555 560
 Gln Ile Glu Thr Leu Val Gln Ser Leu Pro Asp Ile Gln Phe Lys Ile
 565 570 575
 Ala Ala Arg Val Ile Val Ser Asp Arg Leu Ala Gln Met Thr Ile Tyr
 580 585 590
 Pro Asn Val Thr Ile Phe Asn Gly Ile His Tyr Leu Val Asp Val Asp
 595 600 605
 Asn Glu Leu Val Glu Thr Ser Gln Val Leu Leu Asp Ile Asn His Gly
 610 615 620
 Glu Lys Thr Glu Glu Ile Leu Asp Gln Phe Ala Asn Leu Gly Lys Pro
 625 630 635 640
 Ile Leu Ser Phe Glu Asn Thr Lys Thr Tyr Glu Val Gly Gln Glu Ala
 645 650 655
 Tyr Ala Val Asp Gln Val Gln Ala Met Ile Glu Lys Leu Arg Glu Ile
 660 665 670

00765272-112201

Ser Lys

(2) INFORMATION FOR SEQ ID NO: 201:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 910 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201:

CATTCAGAAG CAGACCTATC AAAATCTGGA AATTATTCTT GTTGATGATG GTGCAACAGA 60
 TGAAAGTGGT CGCTTGTGTG ATTCATTCGC TGAACAAGAT GACAGGGTGT CAGTGCTTCA 120
 TAAAAAGAAC GAAGGATTGT CGCAAGCACG AAATGATGGG ATGAAGCAGG CTCACGGGGA 180
 TTATCTGATT TTTATTGACT CAGATGATTA TATCCATCCA GAAATGATTC AGAGCTTATA 240
 TGAGCAATTA GTTCAAGAAG ATGCGGATGT TTCGAGCTGT GGTGTCATGA ATGTCATATG 300
 TAATGATGAA AGCCACAGT CAGCCAATCA GGATGACTAT TTTGTCTGTG ATTCCTAAAC 360
 ATTTCTAAAG GAATACCTCA TAGTGAAAA AATACCTGGG ACGATTTGCA ATAAGCTAAT 420
 CAAGAGACAG ATTGCAACTG CCTATCCTT TCCTAAGGGG TTGATTTACG AAGATGCCTA 480
 TTACCATTTT GATTTAATCA AGTTGGCCAA GAAGTATGTG GTTAATACTA AACCTATTTA 540
 TTACTATTTC CATAGAGGGG ATAGTATTAC GACCAAACCC TATGCAGAGA AGGATTTAGC 600
 CTATATTGAT ATCTACCAAA AGTTTTATAA TGAAGTTGTG AAAAATATC CTGACTTGAA 660
 AGAGGTGCGT TTTTTCAGAT TGGCCTATGC CCACTTCTTT ATTCTGGATA AGATGTGCT 720
 AGATGATCAG TATAAACAGT TTGAAGCCTA TTCTCAGATT CATCGTTTTT TAAAGGCCA 780
 TGCCTTTGCT ATTTCTAGGA ATCCAATTTT CCGTAAGGGG AGAAGAATTA GTGCTTTGGC 840
 CCTATTTCATA AATATTTCCT TATATCGATT CTTATTACTG AAAAATATTG AAAAATCTAA 900
 AAAATTACAT 910

(2) INFORMATION FOR SEQ ID NO:202:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 303 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

Ile Gln Lys Gln Thr Tyr Gln Asn Leu Glu Ile Ile Leu Val Asp Asp
 1 5 10 15

0975572-112004

Gly Ala Thr Asp Glu Ser Gly Arg Leu Cys Asp Ser Ile Ala Glu Gln
 20 25 30
 Asp Asp Arg Val Ser Val Leu His Lys Lys Asn Glu Gly Leu Ser Gln
 35 40 45
 Ala Arg Asn Asp Gly Met Lys Gln Ala His Gly Asp Tyr Leu Ile Phe
 50 55 60
 Ile Asp Ser Asp Asp Tyr Ile His Pro Glu Met Ile Gln Ser Leu Tyr
 65 70 75 80
 Glu Gln Leu Val Gln Glu Asp Ala Asp Val Ser Ser Cys Gly Val Met
 85 90 95
 Asn Val Tyr Ala Asn Asp Glu Ser Pro Gln Ser Ala Asn Gln Asp Asp
 100 105 110
 Tyr Phe Val Cys Asp Ser Gln Thr Phe Leu Lys Glu Tyr Leu Ile Gly
 115 120 125
 Glu Lys Ile Pro Gly Thr Ile Cys Asn Lys Leu Ile Lys Arg Gln Ile
 130 135 140
 Ala Thr Ala Leu Ser Phe Pro Lys Gly Leu Ile Tyr Glu Asp Ala Tyr
 145 150 155 160
 Tyr His Phe Asp Leu Ile Lys Leu Ala Lys Lys Tyr Val Val Asn Thr
 165 170 175
 Lys Pro Tyr Tyr Tyr Tyr Phe His Arg Gly Asp Ser Ile Thr Thr Lys
 180 185
 Pro Tyr Ala Glu Lys Asp Leu Ala Tyr Ile Asp Ile Tyr Gln Lys Phe
 195 200 205
 Tyr Asn Glu Val Val Lys Asn Tyr Pro Asp Leu Lys Glu Val Ala Phe
 210 215 220
 Phe Arg Leu Ala Tyr Ala His Phe Phe Ile Leu Asp Lys Met Leu Leu
 225 230 235 240
 Asp Asp Gln Tyr Lys Gln Phe Glu Ala Tyr Ser Gln Ile His Arg Phe
 245 250 255
 Leu Lys Gly His Ala Phe Ala Ile Ser Arg Asn Pro Ile Phe Arg Lys
 260 265 270
 Gly Arg Arg Ile Ser Ala Leu Ala Leu Phe Ile Asn Ile Ser Leu Tyr
 275 280 285
 Arg Phe Leu Leu Leu Lys Asn Ile Glu Lys Ser Lys Lys Leu His
 290 295 300

(2) INFORMATION FOR SEQ ID NO: 203:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1972 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 203:

TAAGGCTGAT AATCGTGTTC AAATGAGAAC GACGATTAAAT AATGAATCGC CATTGTGTGCT	60
TTCTCCGTTG TATGGCAATG ATAATGGTAA CGGATTATGG TGGGGGAACA CATTGAAGGG	120
AGCATGGGAA GCTATTCTCG AAGATGTAAA GCCATATGCA GCGATTGAAC TTCATCTCTGC	180
AAAAGTCTGT AAACCAACAA GTTGATTCC ACGAGATACG AAAGAATTGA GAGAATGGTA	240
TGTCAGATG TGGAGGAAG CTCAAAGTCT AAACATTCCA GTTTCTTGG TTATTATGTC	300
GGCTGGAGAG CGTAATACAG TTCCTCCAGA GTGTTAGAT GAACAATTCC AAAAGTATAG	360
TGTGTTAAAA GGTGTTTTAA ATATTGAGAA TTATTGGATT TACAATAACC AGTTAGCTCC	420
GCATAGTGCT AAATATTGG AAGTTTGTGC CAAATATGGA GCGCATTTTA TCTGGCATGA	480
TCATGAAAAA TGTTCTGGG AAACATTAT GAATGATCCG ACATCTTTTG AAGCGAGTCA	540
AAAATATCAT AAAAATTGG TGTGGCAAC TAAAAATACG CCAATAAGAG ATGATGCGGG	600
TACAGATTCT ATCGTTAGTG GATTTGGTT GAGTGGCTTA TGTGATAACT GGGGCTCATC	660
AACAGATACA TGGAAATGGT GGGAAAAACA TTATACAAAC ACATTGAAA CTGGAAGAGC	720
TAGGGATATG AGATCCTATG CATCGGAACC AGAATCAATG ATTGCTATGG AAATGATGAA	780
TGTATATACT GGGGGAGGCA CAGTTTATAA TTTGGAATGT SCCGCGTATA CATTTATGAC	840
AAATGATGTA CCAACTCCAG CATTTACTAA AGGTATTATT CTTTCTTTA GACATGCTAT	900
ACAAAATCCA GCTCCAAGTA AGGAAGAAGT TGTAAATAGA ACAAAGCTG TATTTTGGAA	960
TGGAGAAGGT AGGATTAGTT CATTAACCG ATTTTATCAA GGACTTTATT CGAATGATGA	1020
AACAATGCCT TTATATAATA ATGGGAGATA TCATATICTT CCTGTAATAC ATGAGAAAAAT	1080
TGATAAGGAA AAGATTTCAT CTATATCCC TAATGCAAAA ATTTTGACTA AAAATAGTGA	1140
GGAATTGTCT AGTAAAGTCA ACTATTTAAA CTCGCTTTAT CCAAACCTTT ATGAAGGAGA	1200
TGGGTATGCT CAGCGGTAG GTAATTCCTG GTATATTTAT AATAGTAATG CTAATATCAA	1260
TAAAAATCAG CAAGTAATGT TGCCTATGTA TACTAATAAT ACAAGTCGT TATCGTTAGA	1320
TTTGACCCA CATACCTACG CTGTTGTTAA AGAAAAATCA AATAATTTAC ATATTTTATT	1380
GAATAATTAC AGGACAGATA AGACAGCTAT GTGGGCATTA TCAGGAAATT TTGATGCATC	1440
AAAAAGTTGG AAGAAGAAG AATTAGAGTT AGCGAAGTGG ATAAGCAAAA ATTATTCCAT	1500
CAATCCTGTA GATAATGACT TTAGGACAAC AACACTTACA TTAAAAGGGC ATACTGGTCA	1560
TAAACCTCAG ATAAATATAA GTGGCGATAA AAATCATTAT ACTTATACAG AAAATTGGGA	1620
TGAGAATACC CATGTTTATA CCATTACGGT TAATCATAAT GGAATGATAG AGATGTCTAT	1680
AAATACTGAG GGGACAGGTC CAGTCTCTTT CCCAACCA GATAAATTTA ATGATGGTAA	1740
TTTGAATATA GCATATGCAA AACCAACAAC ACAAAGTTCT GTAGATTACA ATGGAGACCC	1800

TAATAGAGCT GTGGATGGTA ACAGAAATGG TAATTTTAAC TCTGGTTCGG TAACACACAC 1860
 TAGGGCAGAT AATCCCTCTT GGTGGGAAGT CGATTGAAA AAAATGGATA AAGTGGGCT 1920
 TGTAAAATT TATAATCGCA CAGATGCTGA GACTCAACGT CTATCTAATT TT 1972

(2) INFORMATION FOR SEQ ID NO:204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 657 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

Lys Ala Asp Asn Arg Val Gln Met Arg Thr Thr Ile Asn Asn Glu Ser
 1 5 10 15
 Pro Leu Leu Leu Ser Pro Leu Tyr Gly Asn Asp Asn Gly Asn Gly Leu
 20 25 30
 Trp Trp Gly Asn Thr Leu Lys Gly Ala Trp Glu Ala Ile Pro Glu Asp
 35 40 45
 Val Lys Pro Tyr Ala Ala Ile Glu Leu His Pro Ala Lys Val Cys Lys
 50 55 60
 Pro Thr Ser Cys Ile Pro Arg Asp Thr Lys Glu Leu Arg Glu Trp Tyr
 65 70 75 80
 Val Lys Met Leu Glu Glu Ala Gln Ser Leu Asn Ile Pro Val Phe Leu
 85 90 95
 Val Ile Met Ser Ala Gly Glu Arg Asn Thr Val Pro Pro Glu Trp Leu
 100 105 110
 Asp Glu Gln Phe Gln Lys Tyr Ser Val Leu Lys Gly Val Leu Asn Ile
 115 120 125
 Glu Asn Tyr Trp Ile Tyr Asn Asn Gln Leu Ala Pro His Ser Ala Lys
 130 135 140
 Tyr Leu Glu Val Cys Ala Lys Tyr Gly Ala His Phe Ile Trp His Asp
 145 150 155 160
 His Glu Lys Trp Phe Trp Glu Thr Ile Met Asn Asp Pro Thr Phe Phe
 165 170 175
 Glu Ala Ser Gln Lys Tyr His Lys Asn Leu Val Leu Ala Thr Lys Asn
 180 185 190
 Thr Pro Ile Arg Asp Asp Ala Gly Thr Asp Ser Ile Val Ser Gly Phe
 195 200 205
 Trp Leu Ser Gly Leu Cys Asp Asn Trp Gly Ser Ser Thr Asp Thr Trp
 210 215 220
 Lys Trp Trp Glu Lys His Tyr Thr Asn Thr Phe Glu Thr Gly Arg Ala

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 102210.2.200000

225 230 235 240
 Arg Asp Met Arg Ser Tyr Ala Ser Glu Pro Glu Ser Met Ile Ala Met
 245 250 255
 Glu Met Met Asn Val Tyr Thr Gly Gly Gly Thr Val Tyr Asn Phe Glu
 260 265 270
 Cys Ala Ala Tyr Thr Phe Met Thr Asn Asp Val Pro Thr Pro Ala Phe
 275 280 285
 Thr Lys Gly Ile Ile Pro Phe Phe Arg His Ala Ile Gln Asn Pro Ala
 290 295 300
 Pro Ser Lys Glu Glu Val Val Asn Arg Thr Lys Ala Val Phe Trp Asn
 305 310 315 320
 Gly Glu Gly Arg Ile Ser Ser Leu Asn Gly Phe Tyr Gln Gly Leu Tyr
 325 330 335
 Ser Asn Asp Glu Thr Met Pro Leu Tyr Asn Asn Gly Arg Tyr His Ile
 340 345 350
 Leu Pro Val Ile His Glu Lys Ile Asp Lys Glu Lys Ile Ser Ser Ile
 355 360 365
 Phe Pro Asn Ala Lys Ile Leu Thr Lys Asn Ser Glu Glu Leu Ser Ser
 370 375 380
 Lys Val Asn Tyr Leu Asn Ser Leu Tyr Pro Lys Leu Tyr Glu Gly Asp
 385 390 395 400
 Gly Tyr Ala Gln Arg Val Gly Asn Ser Trp Tyr Ile Tyr Asn Ser Asn
 405 410 415
 Ala Asn Ile Asn Lys Asn Gln Gln Val Met Leu Pro Met Tyr Thr Asn
 420 425 430
 Asn Thr Lys Ser Leu Ser Leu Asp Leu Thr Pro His Thr Tyr Ala Val
 435 440 445
 Val Lys Glu Asn Pro Asn Asn Leu His Ile Leu Leu Asn Asn Tyr Arg
 450 455 460
 Thr Asp Lys Thr Ala Met Trp Ala Leu Ser Gly Asn Phe Asp Ala Ser
 465 470 475 480
 Lys Ser Trp Lys Lys Glu Glu Leu Glu Leu Ala Asn Trp Ile Ser Lys
 485 490 495
 Asn Tyr Ser Ile Asn Pro Val Asp Asn Asp Phe Arg Thr Thr Thr Leu
 500 505 510
 Thr Leu Lys Gly His Thr Gly His Lys Pro Gln Ile Asn Ile Ser Gly
 515 520 525
 Asp Lys Asn His Tyr Thr Tyr Thr Glu Asn Trp Asp Glu Asn Thr His
 530 535 540
 Val Tyr Thr Ile Thr Val Asn His Asn Gly Met Val Glu Met Ser Ile
 545 550 555 560
 Asn Thr Glu Gly Thr Gly Pro Val Ser Phe Pro Thr Pro Asp Lys Phe

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565

570

575

Asn Asp Gly Asn Leu Asn Ile Ala Tyr Ala Lys Pro Thr Thr Gln Ser
580 585 590

Ser Val Asp Tyr Asn Gly Asp Pro Asn Arg Ala Val Asp Gly Asn Arg
595 600 605

Asn Gly Asn Phe Asn Ser Gly Ser Val Thr His Thr Arg Ala Asp Asn
610 615 620

Pro Ser Trp Trp Glu Val Asp Leu Lys Lys Met Asp Lys Val Gly Leu
625 630 635 640

Val Lys Ile Tyr Asn Arg Thr Asp Ala Glu Thr Gln Arg Leu Ser Asn
645 650 655

Phe

(2) INFORMATION FOR SEQ ID NO: 205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 811 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 205:

CTGTGGCAAT CAGTCAGCTG CTTCCAAACA GTCAGCTTCA GGAACGATTG AGGTGATTTT	60
ACGAGAAAAAT GGCTCTGGGA CACGGGGTGC CTTACACAGAA ATCACAGGGA TTCTCAAAAA	120
AGACGGTGAT AAAAAAATTG ACAACACTGC CAAAACAGCT GTGATTCAAA ATAGTACAGA	180
AGGTGTTCTC TCAGCAGTTC AAGGGAATGC TAATGCTATC GGCTACATCT CCTTGGGATC	240
TTTAACGAAA TCTGTCAAGG CTTTAGAGAT TGATGGTGTC AAGGCTAGTC GAGACACAGT	300
TTTAGATGGT GAATACCCCTC TTCAACGTCC CTTCAACATT GTTTGCTCTT CTAATCTTTC	360
CAAGCTAGGT CAAGATTTTA TCAGCTTTAT CCACTCCAAA CAAGGTCAAC AAGTGGTCAC	420
AGATAATAAA TTTATTGAAG CTA AAAACCGA AACCACGGAA TATACAAGCC AACACTTATC	480
AGGCAAGTTG TCTGTTGTAG GPTCCACTTC AGTATCTTCT TTAATGGAAA AATTAGCAGA	540
AGCTTATAAA AAGAAAAATC CAGAAGTTAC GATTGATATT ACCTCTAATG GGTCTTCAGC	600
AGGTATTACC GCTGTTAAGG AGAAAAACCG TGATATTGGT ATGGTTTCTA GGAATTAAC	660
TCCTGAAGAA GGTAAGAGTC TCACCCATGA TGCTATPGTT TTAGACGGTA TTGCTGTGTG	720
GGTCAATAAT GACAATAAGG CAAGCCAAGT CAGTATGGCT GAACCTGCAG ACGTTTTTAG	780
TGGCAAAATTA ACCACCTGGG ACAAGATTAA A	811

(2) INFORMATION FOR SEQ ID NO: 206:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 270 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

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Cys Gly Asn Gln Ser Ala Ala Ser Lys Gln Ser Ala Ser Gly Thr Ile
 1           5           10          15

Glu Val Ile Ser Arg Glu Asn Gly Ser Gly Thr Arg Gly Ala Phe Thr
 20          25          30

Glu Ile Thr Gly Ile Leu Lys Lys Asp Gly Asp Lys Lys Ile Asp Asn
 35          40          45

Thr Ala Lys Thr Ala Val Ile Gln Asn Ser Thr Glu Gly Val Leu Ser
 50          55          60

Ala Val Gln Gly Asn Ala Asn Ala Ile Gly Tyr Ile Ser Leu Gly Ser
 65          70          75          80

Leu Thr Lys Ser Val Lys Ala Leu Glu Ile Asp Gly Val Lys Ala Ser
 85          90          95

Arg Asp Thr Val Leu Asp Gly Glu Tyr Pro Leu Gln Arg Pro Phe Asn
100         105         110

Ile Val Trp Ser Ser Asn Leu Ser Lys Leu Gly Gln Asp Phe Ile Ser
115         120         125

Phe Ile His Ser Lys Gln Gly Gln Gln Val Val Thr Asp Asn Lys Phe
130         135         140

Ile Glu Ala Lys Thr Glu Thr Thr Glu Tyr Thr Ser Gln His Leu Ser
145         150         155         160

Gly Lys Leu Ser Val Val Gly Ser Thr Ser Val Ser Ser Leu Met Glu
165         170         175

Lys Leu Ala Glu Ala Tyr Lys Lys Glu Asn Pro Glu Val Thr Ile Asp
180         185         190

Ile Thr Ser Asn Gly Ser Ser Ala Gly Ile Thr Ala Val Lys Glu Lys
195         200         205

Thr Ala Asp Ile Gly Met Val Ser Arg Glu Leu Thr Pro Glu Glu Gly
210         215         220

Lys Ser Leu Thr His Asp Ala Ile Ala Leu Asp Gly Ile Ala Val Val
225         230         235         240

Val Asn Asn Asp Asn Lys Ala Ser Gln Val Ser Met Ala Glu Leu Ala
245         250         255

Asp Val Phe Ser Gly Lys Leu Thr Thr Trp Asp Lys Ile Lys
260         265         270

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(2) INFORMATION FOR SEQ ID NO: 207:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 805 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 207:

TTGTCAACAA CAACATGCTA CTTCTGAGGG GACGAATCAA AGGCAAAGCA GTTCAGCGAA 60
 AGTTCCATGG AAAGCTTCAT ACACCAACCT AAACAACCAG GTAAGTACAG AAGAGGTCAA 120
 ATCTCTCTTA TCAGCTCACT TGGATCCAAA TAGTGTGTGAT GCATTTTITA ATCTCGTTAA 180
 TGACTATAAT ACCATTGTCG GCTCAACTGG CTTATCAGGA GATTTCACCT CCTTACTCA 240
 CACCGAATAC GATGTTGAGA AAATCAGTCA TCTCTGGAAT CAAAAGAAGG GCGATTTTGT 300
 TGGGACCAAC TGCCGTATCA ATAGTTATTG TCTTTTGAAA AATTCAGTCA CCATTCCTAAA 360
 GCTTGAAAAA AATGACCACT TGCTTTTCCT AGATAATGAT GCGATTGATA AAGGAAGGTT 420
 CTTTGATTCA CAAGATAAGG AAGAGTTTGA TATTCTATT TCGAGAGTTC CAACTGAGTC 480
 AACTACAGAT GTCAAGGTTT ACGCTGAAAA GATGGAAGCA TTCTTCTCAC AATTTCGAAT 540
 CAATGAAAAA GCTCGAATGC TGTCTGTAGT CTGTCACGAC AATTGGATG GCGAGTATCT 600
 GTTTGTAGGC CACGTTGGGG TCTTAGTACC TGCTGATGAC GGTTCCTTAT TTGTAGAGAA 660
 ATTGACTTTC GAAGAGCCCT ACCAAGCGAT TAAATTTGCT AGTAAGGAAG ATTGCTACAA 720
 GTATTGGGC ACCAAGTATG CGGATTATAC AGGCGAGGGA CTGGCTAAGC CTTTATCAT 780
 GGATAATGAT AAGTGGGTAA AACTT 805

(2) INFORMATION FOR SEQ ID NO:208:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 268 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

Cys Gln Gln Gln His Ala Thr Ser Glu Gly Thr Asn Gln Arg Gln Ser
 1 5 10 15
 Ser Ser Ala Lys Val Pro Trp Lys Ala Ser Tyr Thr Asn Leu Asn Asn
 20 25 30
 Gln Val Ser Thr Glu Glu Val Lys Ser Leu Leu Ser Ala His Leu Asp
 35 40 45
 Pro Asn Ser Val Asp Ala Phe Phe Asn Leu Val Asn Asp Tyr Asn Thr
 50 55 60

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Ile Val Gly Ser Thr Gly Leu Ser Gly Asp Phe Thr Ser Phe Thr His
65                               70                               80

Thr Glu Tyr Asp Val Glu Lys Ile Ser His Leu Trp Asn Gln Lys Lys
85                               90                               95

Gly Asp Phe Val Gly Thr Asn Cys Arg Ile Asn Ser Tyr Cys Leu Leu
100                              105                              110

Lys Asn Ser Val Thr Ile Pro Lys Leu Glu Lys Asn Asp Gln Leu Leu
115                              120                              125

Phe Leu Asp Asn Asp Ala Ile Asp Lys Gly Lys Val Phe Asp Ser Gln
130                              135                              140

Asp Lys Glu Glu Phe Asp Ile Leu Phe Ser Arg Val Pro Thr Glu Ser
145                              150                              155                              160

Thr Thr Asp Val Lys Val His Ala Glu Lys Met Glu Ala Phe Phe Ser
165                              170                              175

Gln Phe Gln Phe Asn Glu Lys Ala Arg Met Leu Ser Val Val Leu His
180                              185                              190

Asp Asn Leu Asp Gly Glu Tyr Leu Phe Val Gly His Val Gly Val Leu
195                              200                              205

Val Pro Ala Asp Asp Gly Phe Leu Phe Val Glu Lys Leu Thr Phe Glu
210                              215                              220

Glu Pro Tyr Gln Ala Ile Lys Phe Ala Ser Lys Glu Asp Cys Tyr Lys
225                              230                              235                              240

Tyr Leu Gly Thr Lys Tyr Ala Asp Tyr Thr Gly Glu Gly Leu Ala Lys
245                              250                              255

Pro Phe Ile Met Asp Asn Asp Lys Trp Val Lys Leu
260                              265

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(2) INFORMATION FOR SEQ ID NO: 209:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 508 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 209:

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TTGTTTCAGGC AAGTCCGTGA CTAGTGAACA CCAACGAAA GATGAAATGA AGACGGAGCA      60
GACAGCTAGT AAAACRAGCG CAGCTAAAGG GAAAGAGGTG GCTGATTTTG AATTGATGGG      120
AGTAGATGGC AAGACCTACC GTTTATCTGA TTACAAGGCG AAGAAAGTCT ATCTCAAATT      180
CTGGGCTTCT TGGTGTTCCT TCTGTCTGCG TAGTCTTCCA GATACGGATG AGATTGCTAA      240
AGAAGCTGGT GATGACTATG TGGTCTTGAC AGTAGTGTC ACGGACATA AGGAGAGCA      300
ATCTGAAGCG GACTTTAAGA ATTGGTATAA GGGATTGGAT TATAAAAATC TCCAGTCCCT      360

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AGTTGACCCA TCAGGCAAAAC TTTTGGAAC TTATGGTGTC CGTTCTTACC CAACCCAAGC 420
 CTTTATAGAC AAAGAAGGCA AGCTGGTCAA AACACATCCA GGATTCATGG AAAAAGATGC 480
 AATTTTGCAA ACTTTGAAGG AATTAGCC 508

(2) INFORMATION FOR SEQ ID NO:210:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

Cys Ser Gly Lys Ser Val Thr Ser Glu His Gln Thr Lys Asp Glu Met
 1 5 10 15
 Lys Thr Glu Gln Thr Ala Ser Lys Thr Ser Ala Ala Lys Gly Lys Glu
 20 25 30
 Val Ala Asp Phe Glu Leu Met Gly Val Asp Gly Lys Thr Tyr Arg Leu
 35 40 45
 Ser Asp Tyr Lys Gly Lys Lys Val Tyr Leu Lys Phe Trp Ala Ser Trp
 50 55 60
 Cys Ser Ile Cys Leu Ala Ser Leu Pro Asp Thr Asp Glu Ile Ala Lys
 65 70 75 80
 Glu Ala Gly Asp Asp Tyr Val Val Leu Thr Val Val Ser Pro Gly His
 85 90 95
 Lys Gly Glu Gln Ser Glu Ala Asp Phe Lys Asn Trp Tyr Lys Gly Leu
 100 105 110
 Asp Tyr Lys Asn Leu Pro Val Leu Val Asp Pro Ser Gly Lys Leu Leu
 115 120 125
 Glu Thr Tyr Gly Val Arg Ser Tyr Pro Thr Gln Ala Phe Ile Asp Lys
 130 135 140
 Glu Gly Lys Leu Val Lys Thr His Pro Gly Phe Met Glu Lys Asp Ala
 145 150 155 160
 Ile Leu Gln Thr Leu Lys Glu Leu Ala
 165

(2) INFORMATION FOR SEQ ID NO: 211:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 994 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 211:

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CTCGCAAAATT GAAAAGGCGG CAGTTAGCCA AGGAGGAAAA GCAGTGAAAA AAACAGAAAT 60
 TAGTAAAGAC GCAGACTTGC ACGAAATTTA TCTAGCTGGA GGTGTTTCT GGGGAGTGG 120
 GGAATATTTT TCACGTGTTT CCGGGGTGAC GGATGCCGTT TCAGGCTATG CAAATGSTAG 180
 AGGAGAAACA ACCAAGTACG AATTGATTAA CCAACAGGT CATGCAGAAA CCGTCCATGT 240
 CACCTATGAT GCCAAGCAAA TTTCTCTCAA GGAATCCTGT CTTCACTATT TCCGCATTAT 300
 CAATCCAACC AGCAAAAATA AACAGGAAA TGATGTGGGG ACCCAGTACC GTACTGGTGT 360
 TTATTACACA GATGACAAGG ATTTGGAAGT GATTAACCAA GTCTTTGATG AGGTGGCTAA 420
 GAAATACGAT CAACCTCTAG CAGTTGAAAA GGAAACTTG AAGAATTTTG TGGTGGCTGA 480
 GGATTACCAT CAAGACTATC TCAAGAAAAA TCCAAATGGC TACTGCCATA TCAATGTTAA 540
 TCAGGCGGCC TATCTGTCTA TTGATGCCAG CAATATCCA AAACCAAGTG ATGAGGAATT 600
 GAAAAAGACC CTGTACCTGT AGGAGTATGC AGTTACCCAG GAAATCAAA CAGAACGAGC 660
 TTTCTCAAAC CGTTACTGGG ATAAATTGTA ATCCGGTATC TATGTGGATA TAGCAACTGG 720
 GGAACCTCTC TTTTCATCAA AAGACAAATT TGAGTCTGGT TGTGGCTGGC CTAGTTTAC 780
 CCAACCCATC AGTCCAGATG TTGTCACCTA CAAGGAAGAT AAGTCCTACA ATATGACGCG 840
 TATGGAAGTG CGGAGCCGAG TAGGAGATTC TCACCTTGGG CATGCTCTTA CGGATGGTCC 900
 ACAGGACAAG GCGGCTTAC GTTACTGTAT CAATAGCCTC TCTATCCGCT TTATTCCTAA 960
 AGACCAATG GAAGAAAAAG GTACGCTTAT TTAC 994

(2) INFORMATION FOR SEQ ID NO:212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

Ser Gln Ile Glu Lys Ala Ala Val Ser Gln Gly Gly Lys Ala Val Lys
 1 5 10 15
 Lys Thr Glu Ile Ser Lys Asp Ala Asp Leu His Glu Ile Tyr Leu Ala
 20 25 30
 Gly Gly Cys Phe Trp Gly Val Glu Glu Tyr Phe Ser Arg Val Pro Gly
 35 40 45
 Val Thr Asp Ala Val Ser Gly Tyr Ala Asn Gly Arg Gly Glu Thr Thr
 50 55 60
 Lys Tyr Glu Leu Ile Asn Gln Thr Gly His Ala Glu Thr Val His Val
 65 70 75 80

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Thr Tyr Asp Ala Lys Gln Ile Ser Leu Lys Glu Ile Leu Leu His Tyr
 85 90 95
 Phe Arg Ile Ile Asn Pro Thr Ser Lys Asn Lys Gln Gly Asn Asp Val
 100 105 110
 Gly Thr Gln Tyr Arg Thr Gly Val Tyr Tyr Thr Asp Asp Lys Asp Leu
 115 120 125
 Glu Val Ile Asn Gln Val Phe Asp Glu Val Ala Lys Lys Tyr Asp Gln
 130 135 140
 Pro Leu Ala Val Glu Lys Glu Asn Leu Lys Asn Phe Val Val Ala Glu
 145 150 155 160
 Asp Tyr His Gln Asp Tyr Leu Lys Lys Asn Pro Asn Gly Tyr Cys His
 165 170 175
 Ile Asn Val Asn Gln Ala Ala Tyr Pro Val Ile Asp Ala Ser Lys Tyr
 180 185 190
 Pro Lys Pro Ser Asp Glu Glu Leu Lys Lys Thr Leu Ser Pro Glu Glu
 195 200 205
 Tyr Ala Val Thr Gln Glu Asn Gln Thr Glu Arg Ala Phe Ser Asn Arg
 210 215 220
 Tyr Trp Asp Lys Phe Glu Ser Gly Ile Tyr Val Asp Ile Ala Thr Gly
 225 230 235 240
 Glu Pro Leu Phe Ser Ser Lys Asp Lys Phe Glu Ser Gly Cys Gly Trp
 245 250 255
 Pro Ser Phe Thr Gln Pro Ile Ser Pro Asp Val Val Thr Tyr Lys Glu
 260 265 270
 Asp Lys Ser Tyr Asn Met Thr Arg Met Glu Val Arg Ser Arg Val Gly
 275 280 285
 Asp Ser His Leu Gly His Val Phe Thr Asp Gly Pro Gln Asp Lys Gly
 290 295 300
 Gly Leu Arg Tyr Cys Ile Asn Ser Leu Ser Ile Arg Phe Ile Pro Lys
 305 310 315 320
 Asp Gln Met Glu Glu Lys Gly Thr Leu Ile Tyr
 325 330

(2) INFORMATION FOR SEQ ID NO: 213:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 625 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 213:

TTGTCAGTCA GGTCTAATG GTTCTCAGTC TGCTGTGGAT GCTATCAAAC AAAAGGGGAA	60
ATTAGTTGTG GCAACCGAGC CTGACTATGC ACCCTTTGAA TTTCATCAT TGGTTGATGG	120

AAAGAACCAG GTAGTCGGTG CAGACATCGA CATGGCTCAG GCTATCGCTG ATGAACCTGG	180
GGTTAAGTTG GAAATCTCAA GCATGAGTTT TGACCAATGTT TTGACCAGTC TTCAAACCTGG	240
TAAGGCTGAC CTAGCAGTTG CAGGAATTAG TGCTACTGAC GAGAGAAAAG AAGTCTTTGA	300
TTTTTCAATC CCATACATATG AAAACAAGAT TAGTTTCTTG GTTCGTAAGG CTGATGTGGA	360
AAAATAACAG GATTTAAC TA GCCTAGAAAG TGCTAATATT GCAGCCCAAA AAGGGACTGT	420
TCCAGAATCA ATGGTCAAGG AACCAATTGCC AAAAGTTCAA TTAACCTCCC TAACATAATAT	480
GGGTGAAGCA GTCAATGAAT TGCAGGCTGG AAAAATAGAT GCTGTTTATA TGGATGAGCC	540
TGTTGCACCT AGTTATGCTG CTA AAAACGC TGGCTTAGCT GTCGCAACTG TCAGCTTGAA	600
GATGAAGGAC GCGACGCCA' ATGCC	625

(2) INFORMATION FOR SEQ ID NO:214:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

Cys	Gln	Ser	Gly	Ser	Asn	Gly	Ser	Gln	Ser	Ala	Val	Asp	Ala	Ile	Lys	1	5	10	15
Gln	Lys	Gly	Lys	Leu	Val	Val	Ala	Thr	Ser	Pro	Asp	Tyr	Ala	Pro	Phe	20	25	30	
Glu	Phe	Gln	Ser	Leu	Val	Asp	Gly	Lys	Asn	Gln	Val	Val	Gly	Ala	Asp	35	40	45	
Ile	Asp	Met	Ala	Gln	Ala	Ile	Ala	Asp	Glu	Leu	Gly	Val	Lys	Leu	Glu	50	55	60	
Ile	Ser	Ser	Met	Ser	Phe	Asp	Asn	Val	Leu	Thr	Ser	Leu	Gln	Thr	Gly	65	70	75	80
Lys	Ala	Asp	Leu	Ala	Val	Ala	Gly	Ile	Ser	Ala	Thr	Asp	Glu	Arg	Lys	85	90	95	
Glu	Val	Phe	Asp	Phe	Ser	Ile	Pro	Tyr	Tyr	Glu	Asn	Lys	Ile	Ser	Phe	100	105	110	
Leu	Val	Arg	Lys	Ala	Asp	Val	Glu	Lys	Tyr	Lys	Asp	Leu	Thr	Ser	Leu	115	120	125	
Glu	Ser	Ala	Asn	Ile	Ala	Ala	Gln	Lys	Gly	Thr	Val	Pro	Glu	Ser	Met	130	135	140	
Val	Lys	Glu	Gln	Leu	Pro	Lys	Val	Gln	Leu	Thr	Ser	Leu	Thr	Asn	Met	145	150	155	160
Gly	Glu	Ala	Val	Asn	Glu	Leu	Gln	Ala	Gly	Lys	Ile	Asp	Ala	Val	His				

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165

170

175

Met Asp Glu Pro Val Ala Leu Ser Tyr Ala Ala Lys Asn Ala Gly Leu
180 185 190

Ala Val Ala Thr Val Ser Leu Lys Met Lys Asp Gly Asp Ala Asn Ala
195 200 205

(2) INFORMATION FOR SEQ ID NO: 215:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3022 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 215:

GGAAACTTCA CAGGATTTTA AAGAGAAGAA AACAGCAGTC ATTAAGGAAA AAGAAGTTGT	60
TAGTAAAAAT CCTGTGATAG ACAATAACAC TAGCAATGAA GAAGCAAAAA TCAAAGAAGA	120
AAATTCCAAT AAATCCCAAG GAGATTATAC GGACTCATTT GTGAATAAAA ACACAGAAAA	180
TCCCAAAAAA GAAGATAAAG TTGTCATATAT TGCTGAATTT AAAGATAAAG AATCTGGAGA	240
AAAAGCAATC AAGGAACATAT CCAGTCTTAA GAATACAAAA GTTTTATATA CTTATGATAG	300
AATTTTAAAC GGTAGTGCCA TAGAAACAAC TCCAGATAAC TTGGACAAAA TTAACAACAT	360
AGAAGGTATT TCATCGGTTG AAAGGGCACA AAAAGTCCAA CCCATGATGA ATCATGCCAG	420
AAAGGAAATT GGAGTTGAGG AAGCTATTGA TTACCTAAG TCTATCAATG CTCCTGTTGG	480
GAAAAATTTT GATGGTAGAG GTATGGTCAT TTCAAATATC GATACTGGAA CAGATTATAG	540
ACATAAGGCT ATGAGAATCG ATGATGATGC CAAAGCCTCA ATGAGATTTA AAAAGAAGA	600
CTTAAAGGC ACTGATAAAA ATTATTGGTT GAGTGATAAA ATCCCTCATG CGTTCAATTA	660
TTATAATGGT GGCAAAATCA CTGTAGAAAA ATATGATGAT GGAAGGGATT ATTTTGACCC	720
ACATGGGATG CATATTGCAG GGATTCTTGC TGGAAATGAT ACTGAACAAG ACATCAAAAA	780
CTTTAACGCG ATAGATGGAA TTGCACCTAA TGCACAAATT TTCTCTTACA AAATGTATTG	840
TGACGCAGGA TCTGGGTTTG CGGGTGATGA AACAAATGTT CATGCTATTG AAGATTCTAT	900
CAACACAAC GTTGATGTTG TTTCGGTATC ATCTGGTTTT ACAGGAACAG GTCTTGTAGG	960
TGAGAAATAT TGGCAAGCTA TTCGGGCATT AAGAAAAGCA GGCATTCCAA TGGTTGTCGC	1020
TACGGGTAACT ATCCGACTT CTGCTTCAAG TTCTTCATGG GATTTAGTAG CAAATAATCA	1080
TCTGAAAATG ACCGACACTG GAAATGTAAC ACGAACTGCA GCACATGAAG ATGCGATAGC	1140
GGTCGCTTCT GCTAAAAATC AAACAGTTGA GTTTGATAAA GTTAACATAG GTGGAGAAAG	1200
TTTTAAATAC AGAAATATAG GGGCCTTTTT CGATAAGAGT AAAATCACAA CAAATGAAGA	1260
TGGAACAAAA GCTCCTAGTA AATTAAAAAT TGTATATATA GGCAAGGGGC AAGACCAAGA	1320

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TTTGATAGGT TTGGATCTTA GGGGCAAAAT TGCAGTAATG GATAGAATTT ATACAAAGGA	1380
TTTAAAAAT GCTTTTAAAA AAGCTATGGA TAAGGGTGCA CGCGCCATTA TGGTTGTAAA	1440
TACTGTAAAT TACTACAATA GAGATAATTG GACAGAGCTT CCAGCTATGG GATATGAAGC	1500
GGATGAAGGT ACTAAAAGTC AAGTGTTC AATTTCAGGA GATGATGGTG TAAAGCTATG	1560
GAACATGATT AATCCTGATA AAAAACTGA AGTCAAAAGA AATAATAAAG AAGATTTTAA	1620
AGATAAATTG GAGCAATACT ATCCAATTGA TATGGAAAGT TTTAATTCCA ACAAACCGAA	1680
TGTAGGTGAC GAAAAAGAGA TTGACTTTAA GTTTGCACCT GACACAGACA RAGAATCTTA	1740
TAAAGAAGAT ATCATCGTTC CAGCAGGATC TACATCTTGG GGGCCAAGAA TAGATTTACT	1800
TTTAAACCC GATGTTTCAG CACCTGGTAA AAATATTAAA TCCACGCTTA ATGTATTATA	1860
TGGCAAATCA ACTTATGGCT ATATGTCAGG AACTAGTATG GCGACTCCAA TCGTGGCAGC	1920
TTCTACTGTT TTGATTAGAC CGAAATTAAA GGAAATGCTT GAAAGACCTG TATTGAAAAA	1980
TCTTAAGGGA GATGACAAAA TAGATCTTAC AAGTCTTACA AAAATTGCCC TACAAAATAC	2040
TGCGCGACCT ATGATGGATG CAACTTCTTG GAAAGAAAAA AGTCAATACT TTGCATCACC	2100
TAGACAACAG GGAGCAGGCC TAATTAATGT GGCCAATGCT TTGAGAAATG AAGTTGTAGC	2160
AACTTTCAAA AACACTGATT CTAAAGGTTT GGTAAACTCA TATGGTTCCA TTTCTCTTAA	2220
AGAAATAAAA GGTGATAAAA AATACTTTAC AATCAAGCTT CACAATACAT CAAACAGACC	2280
TTTGACTTTT AAAGTTTCAG CATCAGCGAT AACTACAGAT TCTCTAATCG ACAGATTAAA	2340
ACTTGATGAA ACATATAAAG ATGAAAAATC TCCAGATGGT AAGCAAAATG TTCCAGAAAT	2400
TCACCCAGAA AAAGTCAAAG GAGCAAAATAT CACATTTGAG CATGATACTT TCACATAGG	2460
CGCAAATTCT AGCTTTGATT TGAATGCGGT TATAAATGTT GGAGAGGCCA AAAACAAAAA	2520
TAAATTTGTA GAATCATTIA TTCAATTTGA GTCAGTGGAA GCGATGGAAG CTCTAAACTC	2580
CAGCGGGGAG AAAATAAACT TCCAACCTTC TTTGTCGATG CCTCTAATGG GATTTGCTGG	2640
GAATTGGAAC CACGAACCAA TCCTTGATAA ATGGGCTTGG GAAGAAGGGT CAAGATCAAA	2700
AACACTGGGA GGTATGATG ATGATGGTAA ACCGAAAATT CCAGGAACCT TAAATAAGGG	2760
AATTGGTGGG GAACATGGTA TAGATAAATT TAATCCAGCA GGAGTTATAC AAAATAGAAA	2820
AGATAAAAAT ACAACATCCC TGGATCAAAA TCCAGAATTA TTTGCTTTCA ATAACGAAGG	2880
GATCAACGCT CCATCATCAA GTGGTTCTAA GATTGCTAAC ATTTATCCTT TAGATTCAAA	2940
TGGAAATCCT CAAGATGCTC AACTTGAAAG AGGATTAACA CCTTCTCCAC TTGTATTAA	3000
AAGTGCAGAA GAAGGATTGA TT	3022

(2) INFORMATION FOR SEQ ID NO:216:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1007 amino acids

075527.01201

(B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

```

Glu Thr Ser Gln Asp Phe Lys Glu Lys Lys Thr Ala Val Ile Lys Glu
 1           5           10          15

Lys Glu Val Val Ser Lys Asn Pro Val Ile Asp Asn Asn Thr Ser Asn
          20           25           30

Glu Glu Ala Lys Ile Lys Glu Glu Asn Ser Asn Lys Ser Gln Gly Asp
          35           40           45

Tyr Thr Asp Ser Phe Val Asn Lys Asn Thr Glu Asn Pro Lys Lys Glu
          50           55           60

Asp Lys Val Val Tyr Ile Ala Glu Phe Lys Asp Lys Glu Ser Gly Glu
          65           70           75           80

Lys Ala Ile Lys Glu Leu Ser Ser Leu Lys Asn Thr Lys Val Leu Tyr
          85           90           95

Thr Tyr Asp Arg Ile Phe Asn Gly Ser Ala Ile Glu Thr Thr Pro Asp
          100          105          110

Asn Leu Asp Lys Ile Lys Gln Ile Glu Gly Ile Ser Ser Val Glu Arg
          115          120          125

Ala Gln Lys Val Gln Pro Met Met Asn His Ala Arg Lys Glu Ile Gly
          130          135          140

Val Glu Glu Ala Ile Asp Tyr Leu Lys Ser Ile Asn Ala Pro Phe Gly
          145          150          155          160

Lys Asn Phe Asp Gly Arg Gly Met Val Ile Ser Asn Ile Asp Thr Gly
          165          170          175

Thr Asp Tyr Arg His Lys Ala Met Arg Ile Asp Asp Asp Ala Lys Ala
          180          185          190

Ser Met Arg Phe Lys Lys Glu Asp Leu Lys Gly Thr Asp Lys Asn Tyr
          195          200          205

Trp Leu Ser Asp Lys Ile Pro His Ala Phe Asn Tyr Tyr Asn Gly Gly
          210          215          220

Lys Ile Thr Val Glu Lys Tyr Asp Asp Gly Arg Asp Tyr Phe Asp Pro
          225          230          235          240

His Gly Met His Ile Ala Gly Ile Leu Ala Gly Asn Asp Thr Glu Gln
          245          250          255

Asp Ile Lys Asn Phe Asn Gly Ile Asp Gly Ile Ala Pro Asn Ala Gln
          260          265          270

Ile Phe Ser Tyr Lys Met Tyr Ser Asp Ala Gly Ser Gly Phe Ala Gly
          275          280          285

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Asp Glu Thr Met Phe His Ala Ile Glu Asp Ser Ile Lys His Asn Val
 290 295 300
 Asp Val Val Ser Val Ser Ser Gly Phe Thr Gly Thr Gly Leu Val Gly
 305 310 315 320
 Glu Lys Tyr Trp Gln Ala Ile Arg Ala Leu Arg Lys Ala Gly Ile Pro
 325 330 335
 Met Val Val Ala Thr Gly Asn Tyr Ala Thr Ser Ala Ser Ser Ser Ser
 340 345 350
 Trp Asp Leu Val Ala Asn Asn His Leu Lys Met Thr Asp Thr Gly Asn
 355 360 365
 Val Thr Arg Thr Ala Ala His Glu Asp Ala Ile Ala Val Ala Ser Ala
 370 375 380
 Lys Asn Gln Thr Val Glu Phe Asp Lys Val Asn Ile Gly Gly Glu Ser
 385 390 395 400
 Phe Lys Tyr Arg Asn Ile Gly Ala Phe Phe Asp Lys Ser Lys Ile Thr
 405 410 415
 Thr Asn Glu Asp Gly Thr Lys Ala Pro Ser Lys Leu Lys Phe Val Tyr
 420 425 430
 Ile Gly Lys Gly Gln Asp Gln Asp Leu Ile Gly Leu Asp Leu Arg Gly
 435 440 445
 Lys Ile Ala Val Met Asp Arg Ile Tyr Thr Lys Asp Leu Lys Asn Ala
 450 455 460
 Phe Lys Lys Ala Met Asp Lys Gly Ala Arg Ala Ile Met Val Val Asn
 465 470 475 480
 Thr Val Asn Tyr Tyr Asn Arg Asp Asn Trp Thr Glu Leu Pro Ala Met
 485 490 495
 Gly Tyr Glu Ala Asp Glu Gly Thr Lys Ser Gln Val Phe Ser Ile Ser
 500 505 510
 Gly Asp Asp Gly Val Lys Leu Trp Asn Met Ile Asn Pro Asp Lys Lys
 515 520 525
 Thr Glu Val Lys Arg Asn Asn Lys Glu Asp Phe Lys Asp Lys Leu Glu
 530 535 540
 Gln Tyr Tyr Pro Ile Asp Met Glu Ser Phe Asn Ser Asn Lys Pro Asn
 545 550 555 560
 Val Gly Asp Glu Lys Glu Ile Asp Phe Lys Phe Ala Pro Asp Thr Asp
 565 570 575
 Lys Glu Leu Tyr Lys Glu Asp Ile Ile Val Pro Ala Gly Ser Thr Ser
 580 585 590
 Trp Gly Pro Arg Ile Asp Leu Leu Leu Lys Pro Asp Val Ser Ala Pro
 595 600 605
 Gly Lys Asn Ile Lys Ser Thr Leu Asn Val Ile Asn Gly Lys Ser Thr
 610 615 620

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Tyr	Gly	Tyr	Met	Ser	Gly	Thr	Ser	Met	Ala	Thr	Pro	Ile	Val	Ala	Ala	625	630	635	640
Ser	Thr	Val	Leu	Ile	Arg	Pro	Lys	Leu	Lys	Glu	Met	Leu	Glu	Arg	Pro	645	650	655	660
Val	Leu	Lys	Asn	Leu	Lys	Gly	Asp	Asp	Lys	Ile	Asp	Leu	Thr	Ser	Leu	660	665	670	675
Thr	Lys	Ile	Ala	Leu	Gln	Asn	Thr	Ala	Arg	Pro	Met	Met	Asp	Ala	Thr	675	680	685	690
Ser	Trp	Lys	Glu	Lys	Ser	Gln	Tyr	Phe	Ala	Ser	Pro	Arg	Gln	Gln	Gly	690	695	700	705
Ala	Gly	Leu	Ile	Asn	Val	Ala	Asn	Ala	Leu	Arg	Asn	Glu	Val	Val	Ala	705	710	715	720
Thr	Phe	Lys	Asn	Thr	Asp	Ser	Lys	Gly	Leu	Val	Asn	Ser	Tyr	Gly	Ser	725	730	735	740
Ile	Ser	Leu	Lys	Glu	Ile	Lys	Gly	Asp	Lys	Lys	Tyr	Phe	Thr	Ile	Lys	740	745	750	755
Leu	His	Asn	Thr	Ser	Asn	Arg	Pro	Leu	Thr	Phe	Lys	Val	Ser	Ala	Ser	755	760	765	770
Ala	Ile	Thr	Thr	Asp	Ser	Leu	Thr	Asp	Arg	Leu	Lys	Leu	Asp	Glu	Thr	770	775	780	785
Tyr	Lys	Asp	Glu	Lys	Ser	Pro	Asp	Gly	Lys	Gln	Ile	Val	Pro	Glu	Ile	785	790	795	800
His	Pro	Glu	Lys	Val	Lys	Gly	Ala	Asn	Ile	Thr	Phe	Glu	His	Asp	Thr	805	810	815	820
Phe	Thr	Ile	Gly	Ala	Asn	Ser	Ser	Phe	Asp	Leu	Asn	Ala	Val	Ile	Asn	820	825	830	835
Val	Gly	Glu	Ala	Lys	Asn	Lys	Asn	Lys	Phe	Val	Glu	Ser	Phe	Ile	His	835	840	845	850
Phe	Glu	Ser	Val	Glu	Ala	Met	Glu	Ala	Leu	Asn	Ser	Ser	Gly	Lys	Lys	850	855	860	865
Ile	Asn	Phe	Gln	Pro	Ser	Leu	Ser	Met	Pro	Leu	Met	Gly	Phe	Ala	Gly	865	870	875	880
Asn	Trp	Asn	His	Glu	Pro	Ile	Leu	Asp	Lys	Trp	Ala	Trp	Glu	Glu	Gly	885	890	895	900
Ser	Arg	Ser	Lys	Thr	Leu	Gly	Gly	Tyr	Asp	Asp	Asp	Gly	Lys	Pro	Lys	900	905	910	915
Ile	Pro	Gly	Thr	Leu	Asn	Lys	Gly	Ile	Gly	Gly	Glu	His	Gly	Ile	Asp	915	920	925	930
Lys	Phe	Asn	Pro	Ala	Gly	Val	Ile	Gln	Asn	Arg	Lys	Asp	Lys	Asn	Thr	930	935	940	945
Thr	Ser	Leu	Asp	Gln	Asn	Pro	Glu	Leu	Phe	Ala	Phe	Asn	Asn	Glu	Gly	945	950	955	960

Ile Asn Ala Pro Ser Ser Ser Gly Ser Lys Ile Ala Asn Ile Tyr Pro
965 970 975

Leu Asp Ser Asn Gly Asn Pro Gln Asp Ala Gln Leu Glu Arg Gly Leu
980 985 990

Thr Pro Ser Pro Leu Val Leu Arg Ser Ala Glu Glu Gly Leu Ile
995 1000 1005

(2) INFORMATION FOR SEQ ID NO: 217:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1696 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 217:

TGTGGTCGAA GTTGAGACTC CTCAATCAAT AACAAATCAG GAGCAAGCTA GGACAGAAAA	60
CCAAGTAGTA GAGACAGAGG AAGCTCCAAA AGAAGAAGCA CCTAAACAG AAGAAAGTCC	120
AAAGGAAGAA CCAAAATCGG AGGTAAAACC TACTGACGAC ACCCTTCCTA AAGTAGAAGA	180
GGGGAAGAA GATTAGCAG AACCAGCTCC AGTTGAAGAA GTAGGTGGAG AAGTTGAGTC	240
AAAACCGAG GAAAAAGTAG CAGTTAAGCC AGAAAGTCAA CCATCAGACA AACCAGCTGA	300
GGAATCAAAA GTTGAACAAG CAGGTGAACC AGTCGCGCCA AGAGAAGACG AAAAGGCACC	360
AGTCGAGCCA GAAAAGCAAC CAGAAGCTCC TGAAGAAGAG AAGGCTGTAG AGGAACACCC	420
GAAACAAGAA GAGTCAACTC CAGATACCAA GGCTGAAGAA ACTGTAGAAC CAAAAGAGGA	480
GACTGTTAAT CAATCTATTG AACAAACCAA AGTTGAACG CCTGCTGTAG AAAAACAAAC	540
AGAACCAACA GAGGAACCAA AAGTTGAACA AGCAGGTGAA CCAGTCGCGC CAAGAGAAGA	600
CGAACAGGCA CCAACGGCAC CAGTTGAGCC AGAAAAGCAA CCAGAAGTTC CTGAAGAAGA	660
GAAGGCTGTA GAGGAACAC CGAAACGAGA AGATAAAATA AAGGGTATTG GTACTAAAGA	720
ACCAGTTGAT AAAAGTGAGT TAAATAATCA AATTGATAAA GCTAGTTCAG TTCTCCTAC	780
TGATTATTCT ACAGCAAGTT ACAATGCTCT TGGACCTGTT TTAGAAACTG CAAAAGGTGT	840
CTATGCTTCA GAGCCTGTAA AACAGCCTGA GGTAAATAGC GAGACAAATA AACTTAAAC	900
GGCTATTGAC GCTCTAAACG TTGATAAAAC TGAATTAAAC AATACGATTG CAGATGCAAA	960
AACAAAGGTA AAAGAACATT ACAGTGATAG AAGTTGGCAA AACCTCCAAA CTGAAGTTAC	1020
AAAGGCTGAA AAGATTGCAG CTAATACAGA TGCTAAACAA AGTGAAGTTA ACGAAGCTGT	1080
TGAAAAATTA ACTGCAACTA TTGAAAAATT GGTGAATTA TCTGAAAGC CAATATTAAC	1140
ATTGACTAGT ACCGATAAGA AATATTGGA ACGTGAAGCT GTTGCTAAGT ATACTCTAGA	1200
AAATCAAAAC AAAACAAAAA TCAATCAAT CACAGCTGAA TTGAAAAAAG GAGAAGAAGT	1260

TATTAATACT GTAGTCCTTA CAGATGACAA GGTAACAACA GAACTATATA GCGCTGCATT 1320
 TAAGAACCCTA GAGTACTACA AAGAATACAC CCTATCTACA ACTATGATTT ACGACAGAGG 1380
 TAACGGTGAA GAACTGAAA CTCTAGAAAA TCAAAATATT CAATTAGATC TTAaaaaaAGT 1440
 TGAGCTTAAA AATATTAAC GTACAGATTT AATCAAATAC GAAATGGAA AAGAACTAA 1500
 TGAATCACTG ATAACAATA TTCCTGATGA TAAGAGCAAT TATTATTAA AAATAACTTC 1560
 AAATAATCAG AAAACTACAT TACTAGCTGT TAAAAATATA GAAGAACTA CGGTTRACGG 1620
 AACACCTGTA TATAAGTTA CAGCAATCGC AGACAATTTA GTCTCTAGAA CTGCTGATAA 1680
 TAAATTGAA GAAGAA 1696

(2) INFORMATION FOR SEQ ID NO:218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 565 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

Val Val Glu Val Glu Thr Pro Gln Ser Ile Thr Asn Gln Glu Gln Ala
 1 5 10 15
 Arg Thr Glu Asn Gln Val Val Glu Thr Glu Glu Ala Pro Lys Glu Glu
 20 25 30
 Ala Pro Lys Thr Glu Glu Ser Pro Lys Glu Glu Pro Lys Ser Glu Val
 35 40 45
 Lys Pro Thr Asp Asp Thr Leu Pro Lys Val Glu Glu Gly Lys Glu Asp
 50 55 60
 Ser Ala Glu Pro Ala Pro Val Glu Glu Val Gly Gly Glu Val Glu Ser
 65 70 75 80
 Lys Pro Glu Glu Lys Val Ala Val Lys Pro Glu Ser Gln Pro Ser Asp
 85 90 95
 Lys Pro Ala Glu Glu Ser Lys Val Glu Gln Ala Gly Glu Pro Val Ala
 100 105 110
 Pro Arg Glu Asp Glu Lys Ala Pro Val Glu Pro Glu Lys Gln Pro Glu
 115 120 125
 Ala Pro Glu Glu Glu Lys Ala Val Glu Glu Thr Pro Lys Gln Glu Glu
 130 135 140
 Ser Thr Pro Asp Thr Lys Ala Glu Glu Thr Val Glu Pro Lys Glu Glu
 145 150 155 160
 Thr Val Asn Gln Ser Ile Glu Gln Pro Lys Val Glu Thr Pro Ala Val
 165 170 175
 Glu Lys Gln Thr Glu Pro Thr Glu Glu Pro Lys Val Glu Gln Ala Gly

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180

185

190

Glu Pro Val Ala Pro Arg Glu Asp Glu Gln Ala Pro Thr Ala Pro Val
 195 200 205
 Glu Pro Glu Lys Gln Pro Glu Val Pro Glu Glu Glu Lys Ala Val Glu
 210 215 220
 Glu Thr Pro Lys Pro Glu Asp Lys Ile Lys Gly Ile Gly Thr Lys Glu
 225 230 235 240
 Pro Val Asp Lys Ser Glu Leu Asn Asn Gln Ile Asp Lys Ala Ser Ser
 245 250 255
 Val Ser Pro Thr Asp Tyr Ser Thr Ala Ser Tyr Asn Ala Leu Gly Pro
 260 265 270
 Val Leu Glu Thr Ala Lys Gly Val Tyr Ala Ser Glu Pro Val Lys Gln
 275 280 285
 Pro Glu Val Asn Ser Glu Thr Asn Lys Leu Lys Thr Ala Ile Asp Ala
 290 295 300
 Leu Asn Val Asp Lys Thr Glu Leu Asn Asn Thr Ile Ala Asp Ala Lys
 305 310 315 320
 Thr Lys Val Lys Glu His Tyr Ser Asp Arg Ser Trp Gln Asn Leu Gln
 325 330 335
 Thr Glu Val Thr Lys Ala Glu Lys Val Ala Ala Asn Thr Asp Ala Lys
 340 345 350
 Gln Ser Glu Val Asn Glu Ala Val Glu Lys Leu Thr Ala Thr Ile Glu
 355 360 365
 Lys Leu Val Glu Leu Ser Glu Lys Pro Ile Leu Thr Leu Thr Ser Thr
 370 375 380
 Asp Lys Lys Ile Leu Glu Arg Glu Ala Val Ala Lys Tyr Thr Leu Glu
 385 390 395 400
 Asn Gln Asn Lys Thr Lys Ile Lys Ser Ile Thr Ala Glu Leu Lys Lys
 405 410 415
 Gly Glu Glu Val Ile Asn Thr Val Val Leu Thr Asp Asp Lys Val Thr
 420 425 430
 Thr Glu Thr Ile Ser Ala Ala Phe Lys Asn Leu Glu Tyr Tyr Lys Glu
 435 440 445
 Tyr Thr Leu Ser Thr Thr Met Ile Tyr Asp Arg Gly Asn Gly Glu Glu
 450 455 460
 Thr Glu Thr Leu Glu Asn Gln Asn Ile Gln Leu Asp Leu Lys Lys Val
 465 470 475 480
 Glu Leu Lys Asn Ile Lys Arg Thr Asp Leu Ile Lys Tyr Glu Asn Gly
 485 490 495
 Lys Glu Thr Asn Glu Ser Leu Ile Thr Thr Ile Pro Asp Asp Lys Ser
 500 505 510
 Asn Tyr Tyr Leu Lys Ile Thr Ser Asn Asn Gln Lys Thr Thr Leu Leu

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515

520

525

Ala Val Lys Asn Ile Glu Glu Thr Thr Val Asn Gly Thr Pro Val Tyr
530 535 540

Lys Val Thr Ala Ile Ala Asp Asn Leu Val Ser Arg Thr Ala Asp Asn
545 550 555 560

Lys Phe Glu Glu Glu
565

(2) INFORMATION FOR SEQ ID NO: 219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1879 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 219:

AACACCTGTA TATAAAGTTA CAGCAATCGC AGACAATTTA GTCTCTAGAA CTGCTGATAA	60
TAAATTTGAA GAAGAATACG TTCACTATAT TGAAAAACCT AAGTCCACG AAGATAATGT	120
ATATTATAAT TTCAAAGAAT TAGTGAAGC TATTCAAAC GATCCTTCAA AAGAATATCG	180
TCTGGGACAA TCAATGAGCG CTAGAAATGT TGTCCTAAT GGAAATCAT ATATCACTAA	240
AGAATTCACA GGAAACTTT TAAGTTCGA AGGAAAACAA TTTGCTATTA CTGAATTGGA	300
ACATCCATTA TTTAATGTGA TAACAAACGC AACGATAAAT AATGTGAATT TTGAAAATGT	360
AGAGATAGAA CGTTCGTGTC AAGATAATAT TGCATCATT GCCAATACTA TGAAAGGTTC	420
TTCAGTTATT ACAAAATGTCA AAATTACAGG CACACTTTCA GTCGTAATA ATGTTGCTGG	480
ATTTGTAAAT AATATGAATG ATGGAACTCG TATTGAAAAT GTTGCTTTCT TTGGCAAACT	540
ACACTCTACA AGTGGAAATG GCTCTCATAC AGGGGGAATT GCAGGTACAA ACTATAGAGG	600
AATTGTTAGA AAAGCATATG TTGATGCTAC TATTACAGGA AACAAAACAC GCGCCAGCTT	660
GTTAGTTCTT AAAGTAGATT ATGGATTAAC TCTAGACCAT CTTATTGGTA CAAAAGCTCT	720
CCTAACTGAG TCGGTTGTAA AAGGTAAAAA AGATGTTTCA AATCCAGTAG AAGTTGGAGC	780
AATAGCAAGT AAGACTTGCG CTGTAGGTAC GGTAAGTAAT TCTGTCAGCT ATGCTAAGAT	840
TATCCGTGGA GAGGAGTTAT TCGGCTCTAA CGACGTTGAT GATTCTGATT ATGCTAGTGC	900
TCATATAAAA GATTTATATG CGGTAGAGGG ATATTCTGCA GGTAATAGAT CATTTAGGAA	960
ATCTAAAACA TTTACTAAAT TAACTAAAGA ACAAGCTGAT GCTAAAGTTA CTACTTTCAA	1020
TATTACTGCT GATAAATTAG AAAGTGATCT ATCTCCTCTT GCAAAACTTA ATGAAGAAAA	1080
AGCCTATTCT AGTATTCAAG ATTATAACGC TGAATATAAC CAAGCCTATA AAAATCTTGA	1140
AAAATTAATA CCATTCTACA ATAAAGATTA TATTGTATAT CAAGGAATA AATTAATAA	1200

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AGAACCCAT CTAATACTA AAGAAGTCTT TCTGTTACC GCGATGAACA ACAATGAGTT 1260
 TATCACAAC CTAGATGAAG CTAATAAAAT TATGTTTAC TATGCGGACG GTACAAAAGA 1320
 TTACTTTAAC TTGCTTCTA GCAGTGAAGG TTTAAGTAAT GTAAAAGAAT ATACTATAAC 1380
 TGACTTAGGA ATTAAATATA CACCTAATAT CGTTCAAAAA GATAACACTA CTCCTGTTAA 1440
 TGATATAAAA TCTATTTTAG AATCAGTAGA GCTTCAGTCT CAAACGATGT ATCAGCATCT 1500
 AAATCGATTA GGTGACTATA GAGTTAATGC AATCAAAGAT TTATATTTAG AAGAAAGCTT 1560
 CACAGATGTT AAAGAAAACCT TAACAAACCT AATCACAAAA TTAGTTCAAA ACGAAGAACA 1620
 TCACTAAAT GATTCTCCAG CTGCTCGTCA AATGATTCGT GATAAAGTCG AGAAAAACAA 1680
 AGCAGCTTTA TTAGTAGGTT TAACTTACCT AAATCGTTAC TATGGAGTTA AATTTGGTGA 1740
 TGTTAATATT AAAGAATTAA TGCTATTCAA ACCAGATTTT TATGGTGAAA AAGTTAGCGT 1800
 ATTAGACAGA TTAATTGAAA TCGGTTCTAA AGAGAACAAC ATTAAGGTTT CACGTACATT 1860
 CGACGCATTC GGTCAGTA 1879

(2) INFORMATION FOR SEQ ID NO:220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 626 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

Thr Pro Val Tyr Lys Val Thr Ala Ile Ala Asp Asn Leu Val Ser Arg
 1 5 10 15
 Thr Ala Asp Asn Lys Phe Glu Glu Glu Tyr Val His Tyr Ile Glu Lys
 20 25 30
 Pro Lys Val His Glu Asp Asn Val Tyr Tyr Asn Phe Lys Glu Leu Val
 35 40 45
 Glu Ala Ile Gln Asn Asp Pro Ser Lys Glu Tyr Arg Leu Gly Gln Ser
 50 55 60
 Met Ser Ala Arg Asn Val Val Pro Asn Gly Lys Ser Tyr Ile Thr Lys
 65 70 75 80
 Glu Phe Thr Gly Lys Leu Leu Ser Ser Glu Gly Lys Gln Phe Ala Ile
 85 90 95
 Thr Glu Leu Glu His Pro Leu Phe Asn Val Ile Thr Asn Ala Thr Ile
 100 105 110
 Asn Asn Val Asn Phe Glu Asn Val Glu Ile Glu Arg Ser Gly Gln Asp
 115 120 125
 Asn Ile Ala Ser Leu Ala Asn Thr Met Lys Gly Ser Ser Val Ile Thr
 130 135 140

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Asn Val Lys Ile Thr Gly Thr Leu Ser Gly Arg Asn Asn Val Ala Gly
 145 150 155 160
 Phe Val Asn Asn Met Asn Asp Gly Thr Arg Ile Glu Asn Val Ala Phe
 165 170 175
 Phe Gly Lys Leu His Ser Thr Ser Gly Asn Gly Ser His Thr Gly Gly
 180 185 190
 Ile Ala Gly Thr Asn Tyr Arg Gly Ile Val Arg Lys Ala Tyr Val Asp
 195 200 205
 Ala Thr Ile Thr Gly Asn Lys Thr Arg Ala Ser Leu Leu Val Pro Lys
 210 215 220
 Val Asp Tyr Gly Leu Thr Leu Asp His Leu Ile Gly Thr Lys Ala Leu
 225 230 235 240
 Leu Thr Glu Ser Val Val Lys Gly Lys Ile Asp Val Ser Asn Pro Val
 245 250 255
 Glu Val Gly Ala Ile Ala Ser Lys Thr Trp Pro Val Gly Thr Val Ser
 260 265 270
 Asn Ser Val Ser Tyr Ala Lys Ile Ile Arg Gly Glu Glu Leu Phe Gly
 275 280 285
 Ser Asn Asp Val Asp Asp Ser Asp Tyr Ala Ser Ala His Ile Lys Asp
 290 295 300
 Leu Tyr Ala Val Glu Gly Tyr Ser Ser Gly Asn Arg Ser Phe Arg Lys
 305 310 315 320
 Ser Lys Thr Phe Thr Lys Leu Thr Lys Glu Gln Ala Asp Ala Lys Val
 325 330 335
 Thr Thr Phe Asn Ile Thr Ala Asp Lys Leu Glu Ser Asp Leu Ser Pro
 340 345 350
 Leu Ala Lys Leu Asn Glu Glu Lys Ala Tyr Ser Ser Ile Gln Asp Tyr
 355 360 365
 Asn Ala Glu Tyr Asn Gln Ala Tyr Lys Asn Leu Glu Lys Leu Ile Pro
 370 375 380
 Phe Tyr Asn Lys Asp Tyr Ile Val Tyr Gln Gly Asn Lys Leu Asn Lys
 385 390 395 400
 Glu His His Leu Asn Thr Lys Glu Val Leu Ser Val Thr Ala Met Asn
 405 410 415
 Asn Asn Glu Phe Ile Thr Asn Leu Asp Glu Ala Asn Lys Ile Ile Val
 420 425 430
 His Tyr Ala Asp Gly Thr Lys Asp Tyr Phe Asn Leu Ser Ser Ser Ser
 435 440 445
 Glu Gly Leu Ser Asn Val Lys Glu Tyr Thr Ile Thr Asp Leu Gly Ile
 450 455 460
 Lys Tyr Thr Pro Asn Ile Val Gln Lys Asp Asn Thr Thr Leu Val Asn
 465 470 475 480

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Asp Ile Lys Ser Ile Leu Glu Ser Val Glu Leu Gln Ser Gln Thr Met
485 490 495

Tyr Gln His Leu Asn Arg Leu Gly Asp Tyr Arg Val Asn Ala Ile Lys
500 505 510

Asp Leu Tyr Leu Glu Glu Ser Phe Thr Asp Val Lys Glu Asn Leu Thr
515 520 525

Asn Leu Ile Thr Lys Leu Val Gln Asn Glu Glu His Gln Leu Asn Asp
530 535 540

Ser Pro Ala Ala Arg Gln Met Ile Arg Asp Lys Val Glu Lys Asn Lys
545 550 555 560

Ala Ala Leu Leu Leu Gly Leu Thr Tyr Leu Asn Arg Tyr Tyr Gly Val
565 570 575

Lys Phe Gly Asp Val Asn Ile Lys Glu Leu Met Leu Phe Lys Pro Asp
580 585 590

Phe Tyr Gly Glu Lys Val Ser Val Leu Asp Arg Leu Ile Glu Ile Gly
595 600 605

Ser Lys Glu Asn Asn Ile Lys Gly Ser Arg Thr Phe Asp Ala Phe Gly
610 615 620

Gln Val
625

(2) INFORMATION FOR SEQ ID NO: 221:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1777 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 221:

ATTAGACAGA TTAATTGAAA TCGGTTCTAA AGAGAACAAC ATTAAAGGTT CACGTACATT	60
CGAGCATTG GGTCAAGTAT TGCCTAAATA TACTAAATCA GGTAAATTAG ATGCATTTTT	120
AAATTATAAT AGACAATTGT TCACAAATAT AGACAATATG AACGATTGGT TTATTGATGC	180
TACAGAAGAC CATGCTCTACA TCGCAGAACG CGCTTCTGAG GTCGAAGAAA TTAATAATTC	240
TAAACATCGT GCATTCGATA ATTTAAACG AAGTCACCTT AGAAATACTA TACTCCCACT	300
ACTGAATATT GATAAAGCAC ATCTTTATTT AATTTCAAAT TATAATGCAG TTGCCTTTGG	360
TATGTCAGAG CGATTAGGTA AAAAATCATT AGAAGATATT AAAGATATCG TTAACAAAGC	420
TGCAGATGGT TATAGAACT ATTATGATTT CTGGTATCGT CTAGCGTCTG ATAACGTATA	480
ACAACGACTA CTAAGAGATG CTGTTATTCC TATTGGGAA GGTATAACG CTCTGGTGG	540
ATGGGTGTA AAATATGGCC GCTATAATAC CGACAAAGTA TATACTCCTC TTAGAGAATT	600

CTTTGGTCCT ATGGATAAGT ATTATAATT AATATGAACA GGAGCTTATG CTGCTATATA 660
 TCCTAACTCT GATGATATTA GAACATGATGT AAAATATGTT CATTAGAAA TGTTGGTGGA 720
 ATACGGTATT TCAGTTTACA CACATGAAAC AACACACGTC AACGACCGTG CGATTTACTT 780
 AGGTGGCTTT GGACACCGTG AAGGTACTGA TGCTGAAGCA TATGCTCAGG GTATGCTACA 840
 AACTCCTGTT ACTGGTAGTG GATTTGATGA GTTTGGTTCT TTAGGTATTA ATATGGTATT 900
 TAAACGCAAA AATGATGGGA ATCAGTGGTA TATTACAGAT CCAAAAATCT TAAAAACAG 960
 AGAAGATATT AATAGATATA TGAAGGGTTA TAATGACACT TTAACCTCTC TTGATGAAAT 1020
 TGAGGCTGAA TCTGTGATTT CTCAACAAAA TAAAGATTTA AATAGTGCAT GGTTCAAAAA 1080
 AATAGATAGA GAATACCGTG ATAACAATAA ATTAAATCAA TGGGATAAAA TTCGAAATCT 1140
 AAGTCAAGAA GAGAAAAATG AATTAAATAT TCAATCTGTT AATGATTTAG TTGATCAACA 1200
 ATTAATGACT AATCGCAATC CAGGTAATGG TATCTATAAA CCCGAAGCAA TTAGCTATAA 1260
 CGATCAATCA CCTTATGTAG GTGTTAGAAT GATGACCGGT ATCTACGGAG GTAATACTAG 1320
 TAAAGGTGCT CCTGGAGCTG TTTCATTCAA ACATAATGCT TTTAGATTAT GGGGTTACTA 1380
 CGGATACGAA AATGGGTTCT TAGGTTATGC TTCAAATAAA TATAACAAC AATCTAAAC 1440
 AGATGGTGAG TCTGTCTCAA GTGATGAATA TATATCAAG AAAATATCTA ACAATACATT 1500
 TAATACTATT GAAGAATTTA AAAAAGCTTA CTTCAAGAA GTTAAAGATA AAGCAACGAA 1560
 AGGATTAACA ACATTCGAAG TAAATGGTTC TTCCGTTTCA TCATACGATG ATTTACTGAC 1620
 ATTGTTTAAA GAAGCTGTTA AAAAAGATGC CGAAACTCTT AAACAAGAG CAAACGGTAA 1680
 TAAACAGTA TCTATGAATA ATACAGTTAA ATTAAGAAG GCTGTTTATA AGAAACTTCT 1740
 TCAACAAACA AATAGCTTTA AAACCTCAAT CTTTAAA 1777

(2) INFORMATION FOR SEQ ID NO:222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 592 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

Leu Asp Arg Leu Ile Glu Ile Gly Ser Lys Glu Asn Asn Ile Lys Gly
 1 5 10 15
 Ser Arg Thr Phe Asp Ala Phe Gly Gln Val Leu Ala Lys Tyr Thr Lys
 20 25 30
 Ser Gly Asn Leu Asp Ala Phe Leu Asn Tyr Asn Arg Gln Leu Phe Thr
 35 40 45
 Asn Ile Asp Asn Met Asn Asp Trp Phe Ile Asp Ala Thr Glu Asp His

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[illegible]

385		390		395		400
Leu Met Thr Asn Arg Asn Pro Gly Asn Gly Ile Tyr Lys Pro Glu Ala						
		405		410		415
Ile Ser Tyr Asn Asp Gln Ser Pro Tyr Val Gly Val Arg Met Met Thr						
		420		425		430
Gly Ile Tyr Gly Gly Asn Thr Ser Lys Gly Ala Pro Gly Ala Val Ser						
		435		440		445
Phe Lys His Asn Ala Phe Arg Leu Trp Gly Tyr Tyr Gly Tyr Glu Asn						
		450		455		460
Gly Phe Leu Gly Tyr Ala Ser Asn Lys Tyr Lys Gln Gln Ser Lys Thr						
		465		470		475
Asp Gly Glu Ser Val Leu Ser Asp Glu Tyr Ile Ile Lys Lys Ile Ser						
		485		490		495
Asn Asn Thr Phe Asn Thr Ile Glu Glu Phe Lys Lys Ala Tyr Phe Lys						
		500		505		510
Glu Val Lys Asp Lys Ala Thr Lys Gly Leu Thr Thr Phe Glu Val Asn						
		515		520		525
Gly Ser Ser Val Ser Ser Tyr Asp Asp Leu Leu Thr Leu Phe Lys Glu						
		530		535		540
Ala Val Lys Lys Asp Ala Glu Thr Leu Lys Gln Glu Ala Asn Gly Asn						
		545		550		555
Lys Thr Val Ser Met Asn Asn Thr Val Lys Leu Lys Glu Ala Val Tyr						
		565		570		575
Lys Lys Leu Leu Gln Gln Thr Asn Ser Phe Lys Thr Ser Ile Phe Lys						
		580		585		590

(2) INFORMATION FOR SEQ ID NO: 223:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 460 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 223:

TAAGACAGAT GAACGGAGCA AGGTGTTTGA CTTTCCATT CCTACTATA CTGCAAAAAA	60
TAAACTCATT GTCAAAAAAT CTGACTTGAC TACTTATCAG TCTGTAAACG ACTTGGCGCA	120
GAAAAAGGTT GGAGCCGAGA AAGGTCGAT TCAAGAGACG ATGGCGAAAG ATTTGCTACA	180
AAATCTCTCC CTCGTATCTC TGCCTAAAAA TGGGAATTTA ATCACAGATT TAAATCAGG	240
ACAAGTGGAT GCCGTTATCT TTGAAGAACC TGTTCACAG GGATTGTGG AAAATAATCC	300
TGATTAGCA ATCGCAGACC TCAATTTTGA AAAAGAGCAA GATGATTCCT ACGCGSTAGC	360
CATgAAAAAA GATAGCAAGA AATTGAAGAG GCAGTTCGAT AAAACCATTC AAAAGTTGAA	420

GGAGTCTGGG GAATTAGACA AACTCATTGA GGAAGCCTTA

460

(2) INFORMATION FOR SEQ ID NO:224:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

```

Lys Thr Asp Glu Arg Ser Lys Val Phe Asp Phe Ser Ile Pro Tyr Tyr
 1             5             10             15

Thr Ala Lys Asn Lys Leu Ile Val Lys Lys Ser Asp Leu Thr Thr Tyr
      20             25             30

Gln Ser Val Asn Asp Leu Ala Gln Lys Lys Val Gly Ala Gln Lys Gly
      35             40             45

Ser Ile Gln Glu Thr Met Ala Lys Asp Leu Leu Gln Asn Ser Ser Leu
      50             55             60

Val Ser Leu Pro Lys Asn Gly Asn Leu Ile Thr Asp Leu Lys Ser Gly
      65             70             75             80

Gln Val Asp Ala Val Ile Phe Glu Glu Pro Val Ser Lys Gly Phe Val
      85             90             95

Glu Asn Asn Pro Asp Leu Ala Ile Ala Asp Leu Asn Phe Glu Lys Glu
      100            105            110

Gln Asp Asp Ser Tyr Ala Val Ala Met Lys Lys Asp Ser Lys Lys Leu
      115            120            125

Lys Arg Gln Phe Asp Lys Thr Ile Gln Lys Leu Lys Glu Ser Gly Glu
      130            135            140

Leu Asp Lys Leu Ile Glu Glu Ala Leu
      145            150

```

(2) INFORMATION FOR SEQ ID NO: 225:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 751 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 225:

```

CTGTGAGAAT CAAGCTACAC CCAAGAGAGAC TAGCGCTCAA AAGACAATCG TCCTTGCTAC      60
AGCTGGCGAC GTGCCACCAT TTGACTACGA AGACAAGGGC AATCTGACAG GCTTTGATAT      120
CGAAGTTTTA AAGCGAGTAG ATGAAAAACT CAGCGACTAC GAGATTCAAT TCCAAAGAAC      180

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CGCCTGGGAG AGCATCTTCC CAGGACTTGA TTCTGGTCAC TATCAGGCTG CGGCCAATAA 240
 CTTGAGTTAC ACAAAGAGC GTGCTGAAAA ATACCTTTAC TCGCTTCCAA TTCCAACAA 300
 TCCCCTCGTC CTGTGTCAGCA ACAAGAAAAA TCCTTTGACT TCTCTTGACC AGATCGCTGG 360
 TAAACAACA CAAGAGGATA CCGGAACCTC TAACGCTCAA TTCATCAATA ACTGGAATCA 420
 GAAACACACT GATAATCCCG CTACAATTAA TTTTCTGGT GAGGATATTG GTAAACGAAT 480
 CCTAGACCTT GCTAACGGAG AGTTTGATTT CCTAGTTTTT GACAAGGTAT CCGTTCAAAA 540
 GATTATCAAG GACCGTGGTT TAGACCTCTC AGTCGTTGAT TTACCTTCTG CAGATAGCCC 600
 CAGCAATTAT ATCATTCTCT CAAGCGACCA AAAAGAGTTT AAAGAGCAAT TTGATAAAGC 660
 GCTCAAGAA CTCTATCAAG ACGGAACCCCT TGA AAAA ACTC AGCAATACCT ATCTAGTGTTG 720
 TTCTTACCTC CCAGATCAAT CTCAGTTACA A 751

(2) INFORMATION FOR SEQ ID NO:226:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

Cys Glu Asn Gln Ala Thr Pro Lys Glu Thr Ser Ala Gln Lys Thr Ile
 1 5 10 15
 Val Leu Ala Thr Ala Gly Asp Val Pro Pro Phe Asp Tyr Glu Asp Lys
 20 25 30
 Gly Asn Leu Thr Gly Phe Asp Ile Glu Val Leu Lys Ala Val Asp Glu
 35 40 45
 Lys Leu Ser Asp Tyr Glu Ile Gln Phe Gln Arg Thr Ala Trp Glu Ser
 50 55 60
 Ile Phe Pro Gly Leu Asp Ser Gly His Tyr Gln Ala Ala Ala Asn Asn
 65 70 75 80
 Leu Ser Tyr Thr Lys Glu Arg Ala Glu Lys Tyr Leu Tyr Ser Leu Pro
 85 90 95
 Ile Ser Asn Asn Pro Leu Val Leu Val Ser Asn Lys Lys Asn Pro Leu
 100 105 110
 Thr Ser Leu Asp Gln Ile Ala Gly Lys Thr Thr Gln Glu Asp Thr Gly
 115 120 125
 Thr Ser Asn Ala Gln Phe Ile Asn Asn Trp Asn Gln Lys His Thr Asp
 130 135 140
 Asn Pro Ala Thr Ile Asn Phe Ser Gly Glu Asp Ile Gly Lys Arg Ile
 145 150 155 160

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Leu Asp Leu Ala Asn Gly Glu Phe Asp Phe Leu Val Phe Asp Lys Val
 165 170 175

Ser Val Gln Lys Ile Ile Lys Asp Arg Gly Leu Asp Leu Ser Val Val
 180 185 190

Asp Leu Pro Ser Ala Asp Ser Pro Ser Asn Tyr Ile Ile Phe Ser Ser
 195 200 205

Asp Gln Lys Glu Phe Lys Glu Gln Phe Asp Lys Ala Leu Lys Glu Leu
 210 215 220

Tyr Gln Asp Gly Thr Leu Glu Lys Leu Ser Asn Thr Tyr Leu Gly Gly
 225 230 235 240

Ser Tyr Leu Pro Asp Gln Ser Gln Leu Gln
 245 250

(2) INFORMATION FOR SEQ ID NO: 227:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 227:

GACTGGATCC TAAATCTAC GACAATAAAA ATC

33

(2) INFORMATION FOR SEQ ID NO: 228:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 228:

CTGAGTCGAC TGGTTGTGCT GGTGAG

27

(2) INFORMATION FOR SEQ ID NO: 229:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 229:

GTCAGGATCC AAATTACAAT ACGGACTATG

30

(2) INFORMATION FOR SEQ ID NO: 230:

00765272.012204

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 230:

CAGTGTCTGAC TAACTCTAGG TCGGAAAC

28

(2) INFORMATION FOR SEQ ID NO: 231:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 231:

GACTGGATCC TGAGAATCAA GCTACACCCA AAGAG

35

(2) INFORMATION FOR SEQ ID NO: 232:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 232:

AGTCAAGCTT TTGTAAGTGA GATTGATCTG G

31

(2) INFORMATION FOR SEQ ID NO: 233:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 233:

GACTGGATCC TGGTAACCGC TCTTCTCGTA ACGCAGC

37

(2) INFORMATION FOR SEQ ID NO: 234:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 234:

AGTCAAGCTT TTTAGGAAC TTTTACGCTT CC

32

(2) INFORMATION FOR SEQ ID NO: 235:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 45 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 235:

AGTCAGATCT TGTGGAAATT TGACAGGTAA CAGCAAAAAA GCTGC

45

(2) INFORMATION FOR SEQ ID NO: 236:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 236:

ACTGAAGCTT TTTGTTTTT CAAGAATCA TCG

33

(2) INFORMATION FOR SEQ ID NO: 237:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 237:

GACTGGATCC TGGTCAAGGA ACTGCTTCTA AAGAC

35

(2) INFORMATION FOR SEQ ID NO: 238:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 32 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 238:

AGTCAAGCTT TCACAAATTC GTTGGTGAAG CC

32

(2) INFORMATION FOR SEQ ID NO: 239:

00765272.012201

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 239:

GA CTGGATCC TAGCTCAGGT GGAACGCTG GTTCATCC

38

(2) INFORMATION FOR SEQ ID NO: 240:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 240:

AGTCAAGCTT ATCAACTTTT CCACCTTCAA CAACC

35

(2) INFORMATION FOR SEQ ID NO: 241:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 241:

GTCAAGATCT CTCCAATAT GGTAAATCTG CGGATGG

37

(2) INFORMATION FOR SEQ ID NO: 242:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 242:

AGTCTGCAG ATCCACATCC GCTTCATCG GGTAAAGAA GG

42

(2) INFORMATION FOR SEQ ID NO: 243:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 243:

GACTGGATCC TGGGAAAAAT TCTAGCGAAA CTAGTGG

37

(2) INFORMATION FOR SEQ ID NO: 244:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 244:

GTCAGTGCAG CTGTCCTTCT TTTACTTCTT TGGTTGC

37

(2) INFORMATION FOR SEQ ID NO: 245:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 245:

GACTGGATCC TGCTAGCGGA AAAAAAGATA CAACTTCTGG

40

(2) INFORMATION FOR SEQ ID NO: 246:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 246:

CTGAAAGCTT TTTTGCCAAT CCTTCAGCAA TCTTGTG

37

(2) INFORMATION FOR SEQ ID NO: 247:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 247:

GACTAGATCT TGGCTCAAAA AATACAGCTT CAAGTCC

37

(2) INFORMATION FOR SEQ ID NO: 248:

0975572.010001

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 248:

AGTCTCTGCAG GTTTTGTGTT GCTTGGTATT GGTCTG

35

(2) INFORMATION FOR SEQ ID NO: 249:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 41 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 249:

GACTGGATCC TAGTACAAAC TCAAGCACTA GTCAGACAGA G

41

(2) INFORMATION FOR SEQ ID NO: 250:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 34 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 250:

CAGTCTGCAG TTCAAAGCT TTTGTATGT CTTC

34

(2) INFORMATION FOR SEQ ID NO: 251:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 37 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 251:

GACTGGATCC TGGCAATTCT GCGGAAGTA AAGATGC

37

(2) INFORMATION FOR SEQ ID NO: 252:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 36 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 252:

AGTCAAGCTT GTTTCATAGC TTTTGTGATT GTTTCG

36

(2) INFORMATION FOR SEQ ID NO: 253:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 253:

GACTGGATCC TTCACAAGAA AAAACAAAAA ATGAAGATGG

40

(2) INFORMATION FOR SEQ ID NO: 254:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 254:

AGTCAAGCTT ATCGACGTAG TCTCCGCCTT C

31

(2) INFORMATION FOR SEQ ID NO: 255:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 255:

GACTGGATCC GAAAGGTCGT TGGTCAAATA ATCTTACC

38

(2) INFORMATION FOR SEQ ID NO: 256:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 256:

AGTCAAGCTT AGAGTTAACA TGGTGCTTGC CAATAGG

37

(2) INFORMATION FOR SEQ ID NO: 257:

09765272-012201

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 37 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 257:

GACTGGATCC AAACCTAGAA AAGAAAGCAG ACAATGC

37

(2) INFORMATION FOR SEQ ID NO: 258:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 36 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 258:

AGTCAAGCTT CCAAACGGT TGATCCAAAC CATCTG

36

(2) INFORMATION FOR SEQ ID NO: 259:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 36 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 259:

GACTGGATCC TTCGAAAGGG TCAGAAGGTG CAGACC

36

(2) INFORMATION FOR SEQ ID NO: 260:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 36 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 260:

AGTCAAGCTT CTGTAGGCTT GGTGTGCCCC AGTTGC

36

(2) INFORMATION FOR SEQ ID NO: 261:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 261:

CTGAGGATCC GGGGATGGCA GCTTTTAAAA ATC

33

(2) INFORMATION FOR SEQ ID NO: 262:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 262:

CAGTAAGCTT GTTACCCAT TCACCATTAC C

31

(2) INFORMATION FOR SEQ ID NO: 263:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 263:

CAGTGGATCC AGACGAGCAA AAAATTAAG

29

(2) INFORMATION FOR SEQ ID NO: 264:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 264:

TCAGAAGCTT GTTACCCAT TCACCATT

28

(2) INFORMATION FOR SEQ ID NO: 265:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 265:

GACTGGATCC CTGTGGTGAG GAAGAACTA AAAAG

35

(2) INFORMATION FOR SEQ ID NO: 266:

09765627-012001

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 266:

CTGAGTCGAC AATATTCTGT AGGAATGCTT CGAATTG

38

(2) INFORMATION FOR SEQ ID NO: 267:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 267:

CTGAGGATCC GACTTTTAAC AATAAACTA TTGAAGAG

38

(2) INFORMATION FOR SEQ ID NO: 268:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 268:

GTCAGTGCAG GTGTGCACCT CCAAAAATCA CGG

33

(2) INFORMATION FOR SEQ ID NO: 269:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 269:

GACTGGATCC CTTTACAGGT AAACAACCTAC AAGTCGG

37

(2) INFORMATION FOR SEQ ID NO: 270:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 270:

CAGTAAGCTT TTCGAAGTTT GGCTCAGAAT TG

32

(2) INFORMATION FOR SEQ ID NO: 271:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 271:

GACTGGATCC CCAGGCTGAT ACAAGTATCG CA

32

(2) INFORMATION FOR SEQ ID NO: 272:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 272:

CAGTAAGCTT ATCTGCAGTA TGGCTAGATG G

31

(2) INFORMATION FOR SEQ ID NO: 273:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 273:

GACTGGATCC GTCTGTATCA TTGAAAACA AAGAAAC

37

(2) INFORMATION FOR SEQ ID NO: 274:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 274:

CAGCTGCAG TTTTACTGTT GCTGTGCTTG TG

32

(2) INFORMATION FOR SEQ ID NO: 275:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 275:

ACTGAGATCTT TGGTCAAAG GAAAGTCAGA CAGGAAAGG

39

(2) INFORMATION FOR SEQ ID NO: 276:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 276:

CAGTAAGCTT ATTCCTGAGC TTTTGTGATA AAGTTGCGC A

41

(2) INFORMATION FOR SEQ ID NO: 277:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 277:

ACTGGGATCC GAAGGATAGA TATATTTTAG CATTGAGAC

40

(2) INFORMATION FOR SEQ ID NO: 278:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 278:

AGTCAAGCTT CCATGGTATC AAAGGCAAGA CTTGG

35

(2) INFORMATION FOR SEQ ID NO: 279:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

00765272-012204

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 279:

GTCAGGATCC GGTAGTTAAA GTTGGTATTA ACGG

34

(2) INFORMATION FOR SEQ ID NO: 280:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 280:

AGTCAAGCTT GCAATTTTGT CGAAGTATTC CAAGAG

36

(2) INFORMATION FOR SEQ ID NO: 281:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 281:

AGTCGGATCC TTCTTACGAG TTGGGACTGT ATCAAGC

37

(2) INFORMATION FOR SEQ ID NO: 282:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 282:

AGTCAAGCTT GTTTATTTTT TCCTTACTTA CAGATGAAGG

40

(2) INFORMATION FOR SEQ ID NO: 283:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 283:

AGTCGGATCC TACTGAGATG CATCATAATC TAGGAGC

37

(2) INFORMATION FOR SEQ ID NO: 284:

0076527-0200

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 37 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 284:

TCAGCTCGAG TTCTTTGACA TCTCCATCAT AAGTCGC

37

(2) INFORMATION FOR SEQ ID NO: 285:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 285:

GACTGGATCC GGTTTTGAGA AAGTATTGTC AGGGG

35

(2) INFORMATION FOR SEQ ID NO: 286:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 39 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 286:

CAGTAAGCTT GGATTTTTTC ATGGATGCAA TTTTTTGG

39

(2) INFORMATION FOR SEQ ID NO: 287:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 43 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 287:

GACTGGATCC GACAACATTT ACTATCCATA CAGTAGAGTC AGC

43

(2) INFORMATION FOR SEQ ID NO: 288:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 40 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

00765272.01201

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 288:

GACTAAGCTT GGCATAAGGT TGCAATTCTG GATTAATTGG

40

(2) INFORMATION FOR SEQ ID NO: 289:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 289:

GACTGGATCC GGCTAAGGAA AGAGTGGATG

30

(2) INFORMATION FOR SEQ ID NO: 290:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 290:

GACTAAGCTT TTCATTTTTA AATTGACTAT GCGCCCG

37

(2) INFORMATION FOR SEQ ID NO: 291:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 291:

GACTGGATCC TTGTTCTTAT GAAGTTGGTC GTCACC

36

(2) INFORMATION FOR SEQ ID NO: 292:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 292:

CATGAAGCTT ATCCTGGATT TTTCCAAGTA AATCT

35

(2) INFORMATION FOR SEQ ID NO: 293:

09765572-042004

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 293:

GACTGGATCC TTATAAGGGT GAATTAGAAA AAGG

34

(2) INFORMATION FOR SEQ ID NO: 294:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 294:

GACTAAGCTT CTTATTAGGA TTGTTAGTAG TTG

33

(2) INFORMATION FOR SEQ ID NO: 295:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 295:

GACTGGATCC GAATGTTGAG GCTCAAGAAA GTTCAGG

37

(2) INFORMATION FOR SEQ ID NO: 296:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 296:

GACTAAGCTT TTCCCCTGAT GGAGCAAAGT AATACC

36

(2) INFORMATION FOR SEQ ID NO: 297:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

0975372.01204

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 297:

GACTGGATCC CTGGGTGTA ACCCATATCC AGCTCCTTCC

40

(2) INFORMATION FOR SEQ ID NO: 298:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 298:

GACTGTCGAC TTCAGCTTGT TTATCTGGGG TTGC

34

(2) INFORMATION FOR SEQ ID NO: 299:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 299:

GACTGGATCC TAGTGATGGT ACTTGGCAAG GAAAAACAG

38

(2) INFORMATION FOR SEQ ID NO: 300:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 300:

ACTGCTGCAG ATCTTTGCCA CCTAGCTTCT CATTG

35

(2) INFORMATION FOR SEQ ID NO: 301:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 301:

GTCAGGATCC TGGGATTCAA TATGTCAGAG ATGATACTAG

40

(2) INFORMATION FOR SEQ ID NO: 302:

0955272-01201

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 302:

CTAGAAGCTT ACGCACCCAT TCACCATTAT CATTG

35

(2) INFORMATION FOR SEQ ID NO: 303:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 303:

GTCAGGATCC GGATAATAGA GAAGCATTAA AAACC

35

(2) INFORMATION FOR SEQ ID NO: 304:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 304:

AGTCAAGCTT GACAAAATCT TGAAACTCCT CTGGTC

36

(2) INFORMATION FOR SEQ ID NO: 305:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 305:

GTCAGGATCC AGATTTTGTG GAGGAGTGTC ATACC

35

(2) INFORMATION FOR SEQ ID NO: 306:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

0976577.012001
102210.2.25595

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 306:

AGTCAAGCTT TCCCTTTTTC CCCTTACGAA TCCAGG

36

(2) INFORMATION FOR SEQ ID NO: 307:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 43 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 307:

GACTGGATCC ATCTGTAGTT TATGCGSATG AACACTTAT TAC

43

(2) INFORMATION FOR SEQ ID NO: 308:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 34 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 308:

GACTGTCGAC GCTTTGGTAG AGATAGAAGT CATG

34

(2) INFORMATION FOR SEQ ID NO: 309:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 38 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 309:

GACTGGATCC TTACTTTGTT ATCGTAGATA CAGCCGGC

38

(2) INFORMATION FOR SEQ ID NO: 310:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 37 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 310:

AGTCAAGCTT TGTTAATGTC GTACCTTCTA AGCGACC__

37

(2) INFORMATION FOR SEQ ID NO: 311:

0075072.01201

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 311:

GACTGGATCC AGCTAAGGTT GCATGGGATG CGATTTCG

37

(2) INFORMATION FOR SEQ ID NO: 312:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 312:

GACTGTCGAC CTGGGCTTTA TTAGTTTGAC TAGC

34

(2) INFORMATION FOR SEQ ID NO: 313:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 313:

CAGTGGATCC CTATCACTAT GTAAATAAAG AGA

33

(2) INFORMATION FOR SEQ ID NO: 314:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 314:

ACTGAAGCTT TTCTGTCCTT GTTTGAGGCA

30

(2) INFORMATION FOR SEQ ID NO: 315:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

00765272-012201

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 315:

CAGTGGATCC TGAGACTCCT CAATCAATAA CAAA

34

(2) INFORMATION FOR SEQ ID NO: 316:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 34 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 316:

ACGTAAGCTT ATAATCAGTA GGAGAAACTG AACT

34

(2) INFORMATION FOR SEQ ID NO: 317:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 317:

CAGTGGATCC GGATGCTCAA GAAACTGCGG

30

(2) INFORMATION FOR SEQ ID NO: 318:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 31 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 318:

GACTAAGCTT TTGCTCTCA TTCTTGCTTC C

31

(2) INFORMATION FOR SEQ ID NO: 319:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 319:

CAGTGGATCC CGACAAAGGT GAGACTGAG

29

(2) INFORMATION FOR SEQ ID NO: 320:

002210.2252260

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 36 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 320:

ACGTAAGCTT ATTTCTTAAT TCAAGTGTTC TCTCTG

36

(2) INFORMATION FOR SEQ ID NO: 321:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 34 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 321:

GACTGGATCC AAATCAATTG GTAGCACAAG ATCC

34

(2) INFORMATION FOR SEQ ID NO: 322:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 322:

CAGTGTGAC ATTAGGAGCC ACTGGTCTC

29

(2) INFORMATION FOR SEQ ID NO: 323:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 31 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 323:

CAGTGGATCC CAAACAGTCA GCTTCAGAA C

31

(2) INFORMATION FOR SEQ ID NO: 324:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

00765272.012201

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 324:

GACTCTGCAG TTAAATCTTG TCCAGGTGG

30

(2) INFORMATION FOR SEQ ID NO: 325:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 325:

GACTGGATCC ATTCGATGAT GCGGATGAAA AG

32

(2) INFORMATION FOR SEQ ID NO: 326:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 326:

GACTAAGCCTT CATTGTCTT TGGGTATTTC GCA

33

(2) INFORMATION FOR SEQ ID NO: 327:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 327:

CAGTGGATCC GGAGAGTCGA TCAAAAGTAG

30

(2) INFORMATION FOR SEQ ID NO: 328:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 328:

GTCAGTGCAG TTGCTCGTCT CGAGGTTG

28

(2) INFORMATION FOR SEQ ID NO: 329:

09765272-012204

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 329:

CAGTGGATCC ATGGACAACA GGAAACTGGG AC

32

(2) INFORMATION FOR SEQ ID NO: 330:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 330:

CAGTAAGCTT ATTAGCTTCT GTACCTGTGT TTG

33

(2) INFORMATION FOR SEQ ID NO: 331:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 41 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 331:

GACTGGATCC CGATGGGCTC AATCCAACCC CAGGTCAAGT C

41

(2) INFORMATION FOR SEQ ID NO: 332:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 332:

GACTCTGCAG CATAGCTTTA TCCTCTGACA TCATCGTATC

40

(2) INFORMATION FOR SEQ ID NO: 333:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

0076527-010034

GACTGGATCC TTCCAATCAA AAACAGGCAG ATGG

34

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

GACTAAGCTT GAGTCCCATA GTCCAAGGCA

30

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 38 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

AGTCGGATCC TATCACAGGA TCGAACGGTA AGACAACC

38

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

ACTGGTCGAC TTCTTTTAAC TCCGCTACTG TGTC

34

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

CAGTGGATCC AAGTTCATCG AAGATGGTTG GGAAGTCC

38

(2) INFORMATION FOR SEQ ID NO: 338:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 32 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 338:

GATCGTCGAC CCGCTCCAC ATGCTCAACC TT

32

(2) INFORMATION FOR SEQ ID NO: 339:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 37 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 339:

TGACGGATCC ATCGTAGCT AGTGAAATGC AAGAAAG

37

(2) INFORMATION FOR SEQ ID NO: 340:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 37 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 340:

TGACAAGCTT ATTCGTTTTT GAAGTAGTTC GTTTCGT

37

(2) INFORMATION FOR SEQ ID NO: 341:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 37 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 341:

GACTGGATCC GCACCAGATG GGGCACAGG TTCAGGG

37

(2) INFORMATION FOR SEQ ID NO: 342:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

00765272-012001

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 342:

TGACAAGCTT AACTTGTAAC GAACAGTTCA ATCTG

35

(2) INFORMATION FOR SEQ ID NO: 343:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 343:

GACTAGATCT TTTTAACCCA ACTGTTGGTA CTTTCC

36

(2) INFORMATION FOR SEQ ID NO: 344:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 344:

TGACAAGCTT GTTAGTGTT ACATTTTGAC CGTC

34

(2) INFORMATION FOR SEQ ID NO: 345:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 345:

ACTGAGATCT TTTTAACCCA ACTGTTGGTA CTTTC

35

(2) INFORMATION FOR SEQ ID NO: 346:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 346:

GACTAAGCTT TCTACGATAA CGATCATTTT CTTTACC

37

(2) INFORMATION FOR SEQ ID NO: 347:

09755272.012004

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 38 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 347:

GA CTGTCGAC TCGTAGATAT TTAAGTCTAA GTGAAGCG

38

(2) INFORMATION FOR SEQ ID NO: 348:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 34 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 348:

AGTCAAGCTT GTTAGTGTT ACATTTTGCA AGTC

34

(2) INFORMATION FOR SEQ ID NO: 349:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 32 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 349:

GACTGGATCC CTTTGGTTTT GAAGGAAGTA AG

32

(2) INFORMATION FOR SEQ ID NO: 350:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 37 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 350:

TGACCTGCAG ACGATTTTTG AAAAATGGAG GIGTATC

37

(2) INFORMATION FOR SEQ ID NO: 351:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 31 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 351:

CAGTGGATCC CTACTACCTC TCGAGAGAAA G

31

(2) INFORMATION FOR SEQ ID NO: 352:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 32 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 352:

ACTGAAGCTT TTCGCTTTT ACTCGTTTGA CA

32

(2) INFORMATION FOR SEQ ID NO: 353:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 42 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 353:

CAGTGGATCC TAAGGTCAA AGTCAGACCG CTAAGAAAGT GC

42

(2) INFORMATION FOR SEQ ID NO: 354:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 38 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 354:

CAGTAAGCTT TAGGGTATCC AAATACTGGT TGTGTATG

38

(2) INFORMATION FOR SEQ ID NO: 355:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 36 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 355:

TGACAGATCT TGACGGGTCT CAGGATCAGA CTCAGG

36

(2) INFORMATION FOR SEQ ID NO: 356:

09765272.01204

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 356:

TGACAAGCTT CAAAGACATC CACCTCTTGA CCTTTG

36

(2) INFORMATION FOR SEQ ID NO: 357:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 357:

GACTGGATCC TAGAGGCTTT GCCAAATGGT GGGAAGGG

38

(2) INFORMATION FOR SEQ ID NO: 358:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 358:

GTCAGTCGAC TTGTTGTAAC ACTTTTCGAG GTTTGGTACC

40

(2) INFORMATION FOR SEQ ID NO: 359:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 359:

CAGTGGATCC TCAAAAAGAG AAGGAAACT TGG

33

(2) INFORMATION FOR SEQ ID NO: 360:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 360:

CAGTCTGCAG TTTCTTCAAC AAACCTTGTT CTTG

34

(2) INFORMATION FOR SEQ ID NO: 361:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 361:

CAGTGGATCC ACGTTCTATT GAGGACCACT T

31

(2) INFORMATION FOR SEQ ID NO: 362:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 362:

CAGTAAGCTT TTCCTTCTCA GTCAATTCTT TTCC

34

(2) INFORMATION FOR SEQ ID NO: 363:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 363:

GACTGGATCC CGCTCAAAT ACCAGAGGTG TTCAG

35

(2) INFORMATION FOR SEQ ID NO: 364:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 364:

GACTAAGCTT AGTACCATGG GTGTGACAGG TTTGAA

36

(2) INFORMATION FOR SEQ ID NO: 365:

0066272.01204
102210"2/25/2000

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 365:

CTGAGGATCC AATTGTACAA TTAGAAAAAG ATAGC

35

(2) INFORMATION FOR SEQ ID NO: 366:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 366:

TGACAAGCTT GCGTTGACTA GGTTCGCAA TGCC

34

(2) INFORMATION FOR SEQ ID NO: 367:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 367:

GACTGGATCC TCTGACCAAG CAAAAGAAG CAGTCAATGA

40

(2) INFORMATION FOR SEQ ID NO: 368:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 368:

TCAGCAGCTG ATCATTGACT TTACGATTG CTCC

34

(2) INFORMATION FOR SEQ ID NO: 369:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 41 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 369:

GACTGGATCC GTCCGGCTCT GTCCAGTCCA CTTTTTCAGC G

41

(2) INFORMATION FOR SEQ ID NO: 370:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 370:

TCAGAAGCTT ATTTTTTGT TCCTTAATGC GTT

33

(2) INFORMATION FOR SEQ ID NO: 371:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 371:

GACTGGATCC GGGACAAATT CAAAAAATA GGCAAGAGG

39

(2) INFORMATION FOR SEQ ID NO: 372:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 372:

GTCAAAGCTT TGGCTCTTIG ATTGCCAACA ACTG

34

(2) INFORMATION FOR SEQ ID NO: 373:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 373:

GACTGGATCC TCGTACCAG CAACAAAGCG AGCAAAGG

39

(2) INFORMATION FOR SEQ ID NO: 374:

0075272-01200

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 374:

GACTAAGCTT ACTTTTTTCT TTTTCCACAC GA

32

(2) INFORMATION FOR SEQ ID NO: 375:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 375:

CAGTGGATCC GAACCGACAA GTCGCCCACT ATCAAGACT

39

(2) INFORMATION FOR SEQ ID NO: 376:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 376:

CTGAAAGCTT TGAATTCTCT TTCTTTTCAG GCT

33

(2) INFORMATION FOR SEQ ID NO: 377:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 377:

TCGAGGATCC GGTGTGCGG TGGCAATATA TCCCGT

36

(2) INFORMATION FOR SEQ ID NO: 378:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 378:

CAGTAAGCTT CCGAACCCAT TCGCCATTAT AGTTGAC

37

(2) INFORMATION FOR SEQ ID NO: 379:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 379:

AGTCGGATCC GGCCAAATCA GAATGGGTAG AAGAC

35

(2) INFORMATION FOR SEQ ID NO: 380:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 380:

TGACCTGCAG CTTCTCATTG ATTTCATCA TCAC

34

(2) INFORMATION FOR SEQ ID NO: 381:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 381:

GACTGGATCC ATTTGCAGAT GATTCTGAAG GATGG

35

(2) INFORMATION FOR SEQ ID NO: 382:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 382:

TCAGCTGCAG CTTAACCCAT TCACATTCT AGTTTAAG

38

(2) INFORMATION FOR SEQ ID NO: 383:

00765273.012301

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 37 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 383:

GACTGGATCC TGTCGCTGCA AATGAACTG AAGTAGC

37

(2) INFORMATION FOR SEQ ID NO: 384:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 34 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 384:

GACTAAGCTT ATACCAAACG CTGACATCTA CGCG

34

(2) INFORMATION FOR SEQ ID NO: 385:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 37 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 385:

AGTCAGATCT TACGTCTCAG CCTACTTTG TAAGAGC

37

(2) INFORMATION FOR SEQ ID NO: 386:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 34 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 386:

GACTAAGCTT AACCCATTCA CCATTGGCAT TGAC

34

(2) INFORMATION FOR SEQ ID NO: 387:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 41 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 387:

CAGTGGATCC TGGACAGGTG AAAGGTCATG CTACATTGT G

41

(2) INFORMATION FOR SEQ ID NO: 388:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 388:

GACTAAGCTT CAACCATTGA GACCTTGCAA CAC

33

(2) INFORMATION FOR SEQ ID NO: 389:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 41 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 389:

GTCAGGATCC GATTGCTCCT TTGAAGGATT TGAGAGAAAC C

41

(2) INFORMATION FOR SEQ ID NO: 390:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 41 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 390:

GACTAAGCTT CGATCAAAGA TAAGATAAT ATATATAAAG T

41

(2) INFORMATION FOR SEQ ID NO: 391:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 47 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 391:

GACTGGATCC TAGGTCATAT GGGACTTTTT TTCTACAACA AAATAGG -

47

(2) INFORMATION FOR SEQ ID NO: 392:

102210.223260

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 37 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 392:

TGACAAGCTT ATCTATCAGC TCATTTAATC GTTTTTCG

37

(2) INFORMATION FOR SEQ ID NO: 393:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 393:

CTGAGGATCC CAACGTTGAG AATTATTTCG GAATG

35

(2) INFORMATION FOR SEQ ID NO: 394:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 31 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 394:

TGACAAGCTT GAGTCTACAA AAGTAATGTA C

31

(2) INFORMATION FOR SEQ ID NO: 395:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 395:

GTCAGGATCC CTAATATCAA TCAAGTTCTT CAGCC

35

(2) INFORMATION FOR SEQ ID NO: 396:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 37 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

00765272.012001

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 396:

TGACAAGCTT GACTGAGGCT TGGACCAGAT TGAAAG

37

(2) INFORMATION FOR SEQ ID NO: 397:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 397:

GACTGGATCC GACAAAAACA TTTAAACGTC CTGAGG

36

(2) INFORMATION FOR SEQ ID NO: 398:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 398:

GACTAAGCTT AGCAGAACT GTGACGCTGG TTCC

34

(2) INFORMATION FOR SEQ ID NO: 399:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 399:

GACTGGATCC TTCTCAGGAG ACCTTTAAAA ATATC

35

(2) INFORMATION FOR SEQ ID NO: 400:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 400:

GACTAAGCTT GTTGGCCATC TTGTACATAC C

31

(2) INFORMATION FOR SEQ ID NO: 401:

09765272.012201

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 401:

GACTGGATCC AGTAAATGCG CAATCAAATT C

31

(2) INFORMATION FOR SEQ ID NO: 402:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 402:

AGTCCTGCAG GTATTTAGCC CAATAATCTA TAAAGCT

37

(2) INFORMATION FOR SEQ ID NO: 403:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 403:

CAGTGGATCC TTACCGCGTT CATCAAGATG TC

32

(2) INFORMATION FOR SEQ ID NO: 404:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 404:

GACTAAGCTT GCCAGATGTT GAAAGAGAG TG

32

(2) INFORMATION FOR SEQ ID NO: 405:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

09765272.042604

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 405:

GACTGGATCC GTGGATGGGC TTAACTATC TTCGTATTCG

40

(2) INFORMATION FOR SEQ ID NO: 406:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 406:

AGTCAAGCTT GCTAGCTTC ACTTCCCTT TCC

33

(2) INFORMATION FOR SEQ ID NO: 407:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 407:

GACTGTCGAC ACTAAACCAG CATCGTTCGC AGGA

34

(2) INFORMATION FOR SEQ ID NO: 408:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 408:

CTGACTGCAG CTTCTGAAG AAATAATGAT TGTGG

35

(2) INFORMATION FOR SEQ ID NO: 409:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 409:

CAGTGGATCC TGACTACCTT GAAATCCCAC TT

32

(2) INFORMATION FOR SEQ ID NO: 410:

00755272-0-00000

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 410:

CAGTAAGCTT TTTTAAAGG TTGTAGAATG ATTTC AATC

39

(2) INFORMATION FOR SEQ ID NO: 411:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 411:

CAGTGTGCGAC TCGTATCTTT TTTGGAGCA ATGTT

35

(2) INFORMATION FOR SEQ ID NO: 412:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 412:

GACTAAGCTT AAATGTTCCG ATACGGGTGA TTG

33

(2) INFORMATION FOR SEQ ID NO: 413:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 413:

CAGTGGATCC GGA CTCTCTC AAGATGTGA AAG

33

(2) INFORMATION FOR SEQ ID NO: 414:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 414:

GACTAAGCTT CTTGAGTTTG TCAAGGATTG CTTT

34

(2) INFORMATION FOR SEQ ID NO: 415:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 415:

CAGTGGATCC CAAGAAATCC TATCATCTCT TCCAGAAG

38

(2) INFORMATION FOR SEQ ID NO: 416:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 416:

GACTAAGCTT TTCAGAACTA AAAGCCGCAG CTT

33

(2) INFORMATION FOR SEQ ID NO: 417:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 417:

GACTGGATCC ACGAAATGCA GGCAGACAG

30

(2) INFORMATION FOR SEQ ID NO: 418:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 418:

CAGTAAGCTT ATCAACATAA TCTAGTAAAT AAGCGT

36

(2) INFORMATION FOR SEQ ID NO: 419:

0976527-012001

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 36 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 419:

CAGTGGATCC TGTATAGTTT TTACGCTTG TTCTTC

36

(2) INFORMATION FOR SEQ ID NO: 420:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 36 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 420:

GTCAAAGCTT TGATAGATG TCATAATCTT CTTAG

36

(2) INFORMATION FOR SEQ ID NO: 421:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 32 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 421:

GACTGGATCC GTGTGTCGAG CATATCTGA AG

32

(2) INFORMATION FOR SEQ ID NO: 422:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 37 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 422:

CAGTAAGCTT ACTTTTACCA TTCTTTGTT CTGCATC

37

(2) INFORMATION FOR SEQ ID NO: 423:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 38 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

102210-2259260

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 423:

GACTGTCGAC GTGTTTGGAT AGCATTCAGA ATCAGACG

38

(2) INFORMATION FOR SEQ ID NO: 424:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 424:

CAGTAAGCTT CGGAAGTAAA GACAATTTTT CC

32

(2) INFORMATION FOR SEQ ID NO: 425:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 425:

CAGTGGATCC GTGCCTAGAT AGTATTATTA CTCAAAC

37

(2) INFORMATION FOR SEQ ID NO: 426:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 426:

GACTAAGCTT TTTGCTTATT TCTCTCAATT TTTC

34

(2) INFORMATION FOR SEQ ID NO: 427:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 427:

CAGTGGATCC CATTGAGAAG CAGACCTATC AAAATC

36

(2) INFORMATION FOR SEQ ID NO: 428:

0976572-01201
102210-222576

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 43 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 428:

ACTGAAGCTT ATGTAATTTT TTAGATTTTT CAATATTTTT CAG

43

(2) INFORMATION FOR SEQ ID NO: 429:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 429:

AGTCGGATCC TAAGGCTGAT AATCGTGTC AAATG

35

(2) INFORMATION FOR SEQ ID NO: 430:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 430:

GACTAAGCTT AAAATTAGAT AGACGTTGAG T

31

(2) INFORMATION FOR SEQ ID NO: 431:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 431:

AGTCGGATCC CTGTGGCAAT CAGTCAGCTG CTTC

35

(2) INFORMATION FOR SEQ ID NO: 432:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

00765272-012201

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 432:

GACTGTCGAC TTTAATCTTG TCCAGGTGG TTAATTTGCC

40

(2) INFORMATION FOR SEQ ID NO: 433:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 38 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 433:

ACTGGTCGAC TTGTCAACAA CAACATGCTA CTTCTGAG

38

(2) INFORMATION FOR SEQ ID NO: 434:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 434:

GACTCTGCAG AAGTTTAACC CACTTATCAT TATCC

35

(2) INFORMATION FOR SEQ ID NO: 435:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 435:

ACTGGGATCC TTGTTCAGCG AAGTCGTGA CTAGTGAAC

39

(2) INFORMATION FOR SEQ ID NO: 436:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 436:

GACTAAGCTT GGCTAATTCC TTCAAAGTTT GCA

33

(2) INFORMATION FOR SEQ ID NO: 437:

09765272.012204

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 437:

AGTCGGATCC CTCGCAAAATT GAAAAGGCGG CAGTTAGCC

39

(2) INFORMATION FOR SEQ ID NO: 438:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 438:

GACTAAGCTT GTAAATAAGC GTACCTTTTT CTTC

35

(2) INFORMATION FOR SEQ ID NO: 439:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 38 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 439:

TCAGGGATCC TTGTCACTCA GGTCTAATG GTTCTCAG

38

(2) INFORMATION FOR SEQ ID NO: 440:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 440:

AGTCAAGCTT GGCATTGGCG TCGCCGTCTC TC

32

(2) INFORMATION FOR SEQ ID NO: 441:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 38 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

09755272-012201

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 441:

GACTGGATCC GGAACTTCA CAGGATTTTA AAGAGAAG

38

(2) INFORMATION FOR SEQ ID NO: 442:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 442:

GACTGTCGAC AATCAATCCT TCCTCTGCAC TTCT

34

(2) INFORMATION FOR SEQ ID NO: 443:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 443:

CAGTGGATCC TGTGGTCGAA GTTGAGACTC CTCAATC

37

(2) INFORMATION FOR SEQ ID NO: 444:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 444:

GACTAAGCTT TTCTTCAAAT TTATTATCAG C

31

(2) INFORMATION FOR SEQ ID NO: 445:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 445:

AGTCGGATCC AACACCTGTA TATAAGTTA CAGCAATCG

39

(2) INFORMATION FOR SEQ ID NO: 446:

00765273-013604

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 37 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 446:

GACTGTCGAC TACTTGACCG AATGCGTCGA ATGTACG

37

(2) INFORMATION FOR SEQ ID NO: 447:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 34 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 447:

CTGAGGATCC ATTAGACAGA TTAATTGAAA TCGG

34

(2) INFORMATION FOR SEQ ID NO: 448:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 34 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 448:

GACTGTCGAC TTAAAGATT GAAGTTTAA AGCT

34

(2) INFORMATION FOR SEQ ID NO: 449:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 449:

TGACGGATCC TAAGACAGAT GAACGGAGCA AGGTG

35

(2) INFORMATION FOR SEQ ID NO: 450:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

0975572-012001
102210-222526

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 450:

CTGAAAGCTT TAAGGCTTCC TCAATGAGTT TGTCT

35

(2) INFORMATION FOR SEQ ID NO: 451:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 451:

GACTGGATCC CTGTGAGAAT CAAGCTACAC CCA

33

(2) INFORMATION FOR SEQ ID NO: 452:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 452:

CTGAAAGCTT TTGTAAGTGA GATTGATCTG GGAG

34